Aay66213 HLA-A11-b

AAY66213

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Abp53932 VEGFR-3 b
Abp53931 VEGFR-3 b
Abp5396 VEGFR-3 b
Abj04461 Stem cell
Abj04461 Stem cell
Abj04463 Stem cell
Abj04463 Inorine-
Abj04531 Molt-4 le
Abj03715 Fluorine-
Aay03715 Fluorine-
Aay03715 Immunogen
Abp5396 VEGFR-3 b
Adg94005 Immunogen
Adj80014 Peptide h
Abb6396 VEGFR-3 b
Adg94005 Immunogen
Abp6396 VEGFR-3 b
Adg94005 Immunogen
Abp6396 VEGFR-3 b
Adg94005 Immunogen
Abb6607 Desmocoll
Abb6607 Desmocoll
Abb6607 Desmocoll
Abb6607 Insulin/i
Aau90541 Insulin/i
Aaw3066 Specific
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                            December 30, 2004, 14:21:47 ; Search time 93.3333 Seconds (without alignments) 38.435 Million cell updates/sec
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Compugen Ltd.
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GenCore version
(c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
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ABP53968
ABJ04461
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ABJ04531
ABJ04531
ABP53964
AAY03115
ADG94005
ADG94005
ADG94005
ADB94606
ABB46366
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                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp201s:*
6: geneseqp2003s:*
7: geneseqp2003as:*
7: geneseqp2003bs:*
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                                                                                                                               1 CGYWLTIWGC 10
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Perfect score:
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AAY76794 ABP53418 ABP22609 ABP20314

AAU90543 AAU90464 AAU90541 AAW43886 AAY66209

26	Homo sapiens. Synthetic. XX X
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(LUDW-) LUDWIG INST (
(LICN ) LICENTIA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                      GYWLTIWG
                                                                                                                                             present invention
                                                                                                                                                                                                                                                                                                                                        2 GYWLTIWG
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                                                                                                                                                                                             Sequence 10 AA;
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                                                                                                                                                                                                                                           Query Match
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Matches
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          pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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spleen, kidney, lymph node, small intestine, blood cells,
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                                                                                                                                                                                                                                             Length 10;
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                                                                                                                                                                                                                                           100.0%; Score 72; DB 5; 100.0%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                             Mismatches
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nes 10; Conservative
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                                                                                                                                                                                             Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotenaive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. Hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
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                                                                                                                                                                                           Length 10;
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0.67;
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                                                                                                                                                                                                                               0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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100.0%;
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                                                                                                                                                                                                             Local Similarity 100.
Les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breat, endometrium, prostate, testicle, over skin, head and neckynages, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of targeting peptides that can be used to treate.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid of Selective Ligands) method comprises a single differential
                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                 Score 50, DB 5, Length 10, Pred. No. 2.3; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stem cell (mesenchymal) targeting peptide 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 76; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ04472 standard; peptide; 9 AA
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                            Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The SRASIL method of the invention involves: exposing the first phase to a second display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phase in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides in recovery of specific phage and a convention are useful for treating disease states, such as: diabetes; inflammatory arthritis, atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardlovascular disease and degenerative disease. The present mino acid sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                           BRASIL, targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential centrifugation step.
                                                                                                        Gaps
                                                                                                        1,
                                                                      Length 9;
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                                                                                                        Indels
                                                                     Score 39.5; DB 5;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                           Stem cell (mesenchymal) targeting peptide 50.
                                                                                                        1; Mismatches
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targeting peptide of the invention
                                                                                                                                                                                                                                                                   ABJ04461 standard; peptide; 9 AA.
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17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                                                                                                                                                                        24-OCT-2002 (first entry)
                                                                                                        6; Conservative
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                                                                 Query Match
Best Local Similarity
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                                   Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                        Matches
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BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
                                                                                                                                  Molt-4 leukaemia cell line targeting peptide 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 79; Page 100; 167pp; English.
                                          ABJ04531 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                07-SEP-2001; 2001WO-US028124.
                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-0231266P
17-JAN-2001; 2001US-00765101
                                                                                                      24-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-404697/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  centrifugation step
                                                                                                                                                                                                                                                                       WO200220822-A2
                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                   14-MAR-2002
                                                                        ABJ04531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
            RESULT 7
                            ABJ04531
                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from unbound phage in a single differential centrifugation from the remaining unbound phage in a single differential centrifugation method shows a significant increase in recovery of specific phage and substantial decrease in background. The BRASIL method is useful for teathod of the invention are useful for tranting opptides identified by the method of the invention are useful for tranting disease states, such as: diabetes; inflammatory arthritis, atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and
ï
                                                                                                                                                                                                                                                    BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analyais of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degenerative disease. The present amino acid sequence represents a targeting peptide of the invention {\sf res}
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2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 5; Length 9; Pred. No. 1.7e+06; 1; Mismatches 3; Indels
                                                                                                                                                                                                                           Stem cell (mesenchymal) targeting peptide 49.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 76; 167pp; English.
                                                                                                                                   ABJ04460 standard; peptide; 9 AA.
5.
                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2001; 2001WO-US028124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.6%;
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM.
5; Conservative
                            1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasqualini R;
                                                        CGWW-GLWPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-404697/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        centrifugation step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              WO200220822-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                 Jnidentified.
                                                                                                                                                                                             24-OCT-2002
                                                                                                                                                                 ABJ04460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
Matches
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The SRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides; in action is useful for targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease, bacterial infection; viral infection; cardiovascular disease and degenerative disease. The present amino acid sequence represents a reger are a reger in a regeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 33.5; DB 5;
50.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP53964 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
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Gaps

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3; Indels

4; Conservative

| :| | | CDWWTTAW 8 CGYWLTIW 8

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'note= "N-terminal acetylation; optionally has a free or

protected thiol group"

Location/Qualifiers

/note= "D-form residue; optionally has a free or protected thiol group"

note= "D-form residue" /note= "D-form residue"

98WO-US018268.

'note= "D-form residue" note= "D-form residue"

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18F radionuclide, targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radiolabeling thiol-containing peptides with fluorine-18.
              Fluorine-18 (F-18) labeled peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-228967/19.
                                                                                                                                                       Misc-difference
                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffithe GL;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9911590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1999.
                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) and eve cytostatic, hepatotropic, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, compositions and methods from the present invention are useful for compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, there, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oseophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence
                                                                                              angiogenesis, lymphangiogenesis, vascular endothelial growth factor, cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; unnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                 Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                /note= "X is any amino acid"
                                                VEGFR-3 binding peptide SEQ ID NO:67.
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 81; 149pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002; 2002WO-IB000099
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001US-0262476P.
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alitalo K, Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-691521/74.
                                                                                                                                                                                                                                                                               Misc-difference 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention
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                                                                                                                                                                                                                                                                                                                                   WO200257299-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
                                                                                                                                                                                                         Homo sapiens.
Synthetic.
              09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2002
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The invention traders to a mechanical positron

chical population traders to a mechanical positron

chical population traders of a mechanical positron

chical fluorinated alkene in which at least one of the two double bonded carbon

chow with a labeling reagent of formula: 18r (CH2)n-CRIR2-(CH2)n-X, or a

fluorinated alkene in which at least one of the two double bonded carbon

chome bears at least one leaving group comprising I, Br, Cl, azide,

cosylate, mesylate, mosylate, nosylate, triflate, maleimide

coptionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I,

Br, Cl, azide, tosylate, mesylate, nosylate, triflate, m. CONH2, COOH,

CM, sulfonic acid, tertiary amine, quaternary ammonium, alkyl (optionally

substituted by CONH2, COON, OH, sulfonic acid, tertiary amine or

chargeted by CONH2, COON, CONN'2 or CON'; and R' = 1-6c alkyl or

phenyl. The method is used for Radiolabeling peptide-containing targeting

vectors such as proteins, antibodies, antibody fragments and receptor-

targeted peptides for use in routine clinical positron emission

comography. The method is simple and efficient. The method uses the

cunique property of the free thiol groups which are rapidly alkylated at

neutral pH and moderate temperatures. Sequences AAY03714-716 represent

examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                              a method for incorporating 18F radionuclide into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.8%; Score 33; DB 2; Length 8; ilarity 100.0%; Pred. No. 1.7e+06; Conservative 0; Mismatches 0; Indels
Claim 14; Page 15; 22pp; English.
                                                                                    invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
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AAY03715 standard; peptide; 8 AA.

AAY03715 ID AAY

GYWXXXW

ઠે 셤 08-JUN-1999 (first entry)

AAY03715;

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CGYW

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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising adminstering a bi-specific diseased tissues in a patient comprising adminstering a bi-specific cartibody (or fragment) having at at least 1 arm (A) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion to roteins are useful for pre-targetling methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method
                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                     'note= "acetylated; modified with free amino acid group,
                                                                                                                                                                                                                                                                                    protected amino acid group, chelating agent or a metal-
chelate complex"
                                                                                                                                                  Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bi-specific antibodies that bind specific target tissue and targeted conjugates.
                                                                                                                 Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansen HJ, Griffiths GL, Leung S, Mcbride WJ,
                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                       note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "D-form residue"
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page 61; 76pp; English.
                 AAY76817 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US013879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0090142P
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                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-160561/14.
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1998;
                                                                                 28-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                    Synthetic
                                                  AAY76817;
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oscophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence represents a specifically claimed VEGR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor receptor 3 inhibitor; VBGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PBGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                  Gaps
                                  ;
 DB 3; Length 8;
                 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "X is any amino acid"
45.8%; Score 33; DB 100.0%; Pred. No. 1.7; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "any amino acid"
                                                                                                                                                                                                                                                                                         VEGFR-3 binding peptide SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 81; 149pp; English.
                                                                                                                                                                                     ABP53965 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2002; 2002WO-IB000099,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001US-0262476P.
                                                                                                                                                                                                                                                        09-JAN-2003 (first entry)
                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-691521/74.
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 4.
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                                                                    1 CGYW 4
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CGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                      ABP53965;
                                                                                                                                                      RESULT 11
                                                                                                                                                                       ABP53965
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Sequence 8 AA

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in the method of the invention.
                     Sequence 8 AA;
                                                                                    CGYW
                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-2004
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                  ADL98014;
                                                                                    <del>.</del>
                                         Query Match
                                                              Matches
                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to targeting an agent towards a target site in a tissue, comprising administering to the tissue, a multi-specific antibody or its fragment, comprising a targeting arm that binds to an antigen of the target site and a capture arm that binds to an antigen of administering a polymer conjugate that binds to the capture arm, the conjugate has a polymer conjugate (or the agent such as therapeutic agent, a peptide, an enzyme and a labelled ligand. Also included is a kit useful for targeting a target site within a tissue in a subject or tissue sample comprising the above mentioned multi-specific antibody or its fragment and a polymer conjugate. The method is used for targeting an agent towards a target site in a tissue (e.g. a tumour). The method is also useful for therapputic or diagnostic purposes and further in photodynamic therapy. The present sequence is an immunogenic peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Targeting an agent towards a target site in a tissue, by administering in a tissue, a multi-specific antibody or its fragment and a polymer conjugate that binds to the capture arm of the multi-specific antibody.
                                                                                                                                                                                                               peptide; multi-specific antibody; polymer conjugate; tumour;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                        note= "optionally methylated or Acetylated D-form
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                                                                                                                                                                                                                                                                                         'note= "Optionally methylated or Acetylated"
        Score 33; DB 5; Length 8; Pred. No. 1.7e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "D-form residue"
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 19pp; English
                                                                                                                                                                                                                           photodynamic therapy.
                                                                                                                           ADG94005 standard; peptide; 8 AA
        45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2001; 2001US-0308605P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2002; 2002US-00209592
                                                                                                                                                                     (first entry)
                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                   residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-801085/75.
                                                                                                                                                                                           Immunogenic peptide
     Query Match
Best Local Similarity
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                                                                       GYWXXXW
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                                                                                                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                     11-MAR-2004
                                                                                                                                                                                                                Immunogenic
                                                                                                                                                                                                                          cytostatic;
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                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                ADG94005;
                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  photodynamic diagnosis; cancer; tumour; cardiovascular lesion; inflammatory disease; neurodegenerative disease; metabolic disease; inflammatory disease; b-cell malignancy; Alzheimer's disease; amyloidosis; autoimmune disease; bacterial infection; fungal infection; parasitic infection; viral infection; carcinoembryonic antigen-expressing tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating cancer and metabolic diseases by administering a multi-specific antibody having a targeting arm that binds to an antigen and a capture arm that binds to a polymer conjugate comprising a therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of diagnosing or treating a disease or disorder. The method involves administering to a tissue a multi-specific antibody (I) or antibody fragment, comprising a targeting arm that binds to an antigen on the target site, and a capture arm that binds to a
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Optionally Cysteinyl; if Cys the residue is methylated; N-terminal acetylated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Optionally Cysteinyl; if Cys the residue is methylated; N-terminal acetylated."
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45.8%; Score 33; DB 7; L
100.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                           ADL98014 standard; peptide; 8 AA.
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31-JUL-2002; 2002US-00209592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004 (first entry)
                           Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide hapten #2.
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Sequence 8 AA;

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Corribona, lung carcinoma, intestinal carcinoma (preferably renal carcinoma, intestinal carcinoma, and astroam and astroam, intestinal carcinoma, and astroam and astroam and astroam metabolic disease.

Corribona, lung carcinoma, intestinal carcinoma (preferably renal carcinoma, intestinal carcinoma, and astroam astroam astroam and astroam astroam and astroam and astroam astroa polymer conjugate, and administering to the tissue a polymer conjugate that binds to the capture arm, the polymer conjugate comprising a polymer conjugated to a diagnostic or therapeutic agent. Also included is a method for photodynamic diagnosis or treatment of a disease or disorder; influenzae B, Treponema pallidum, Lyme disease spirochetes, Pseudomonas aeruginosa, Mycobacterium leprae, Brucella abortus, Mycobacterium tuberculosis, and Tetanus toxin. The infectious disease is caused by a protozoa chosen from Plasmodium falciparum, Plasmodium vivax, Toxoplasma gondii, Trypanosoma rangeli , Trypanosoma cruzi, Trypanosoma rhodesiensei, Trypanosoma brucei, Schistosoma mansoni, Schistosoma rhodesiensei, Trypanosoma brucei, Schistosoma mansoni, Schistosoma banicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus, Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, Theileria parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinococcus granulosus, and Mesocestoides corti. The infectious disease is caused by a mycoplasma chosen from Mycoplasma arthritidis, M. hyorhinis, M. orale, M. årginini, Acholeplasma faidlawii, M. salivarum and M. pneumoniae. The cancer is preferably chosen from carcinoembryonic antigen (CBA)-expressing malignancy. The present sequence represents a peptide used in the method of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polypreptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                      Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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Pred. No. 4.6e+02;
                             Indels
Length 8;
                                                                                                                                                                                                                                                                        Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.
              1.7e+06;
DB 8;
                             0; Mismatches
                Pred. No.
 45.8%; Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 101; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gour BJ;
                                                                                                                                                                            ABB46346 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2000; 2000US-00535852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001; 2001WO-IB001400.
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                  100.0%;
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Best Local Similarity 60..
Best Grand Grandstive
                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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CGYALDARGC 10

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RESULT 15

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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45141-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polymucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                          Desmosomal cadherin, cell adhesion, CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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Best Local Similarity 60.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 4;
                                                                                                                                     Desmocollin-1 CAR cyclic peptide 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 109; 127pp; English.
                  ABB46607 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001; 2001WO-IB001400.
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ABB46607
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Search completed: December 30, 2004, 14:38:07 Job time : 103.333 secs

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Sequence 1, Appli
Sequence 22, Appl
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Sequence 1352, Ap
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|: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-520-535-1352

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US-09-311-784A-374

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US-09-30-497A-110

US-09-108-709-22

US-09-108-709-22

US-09-108-709-22

US-09-108-709-22

US-09-108-709-22

US-09-108-709-22

US-09-108-708-110

US-09-108-725-10

US-09-108-725-10

US-09-111-784A-348

US-08-135-253-13

US-08-315-253-13

US-08-315-253-13

US-08-315-738-21

US-08-315-748-119

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US-08-315-748-119
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 1495, Ap
Sequence 1495, Ap
Sequence 1495, Ap
Sequence 150, Appl
Sequence 1587, Ap
Sequence 1587, Appl
Sequence 1357, Appl
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42, Appl
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1095
Sequence 1095
Sequence 108, Application US/09535852
Setent No. 6538911
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
ITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
ITLE OF INVENTION: DESMOSOVAL CADHERIN-MEDIATED FUNCTIONS
FILE REPERRACE: 100086, 407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWAREN FRAESEQ for Windows Version 4.0
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1352, Application US/09535852

Patent No. 653811

GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
ITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100066.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARET PRESERVE
SEQ ID NO 1352
LENGTH: 10
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             4.
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Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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ORGANISM: Artificial Sequence
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                     1 CGYWLTIWGC 10
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Best Local Similarity
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; ORGANISM: Human immunodeficiency virus US-08-986-234-92
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; Sequence 374, Application US/09311784A
; Patent No. 6534482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.7%;
80.0%;
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Best Local Similarity 80.0
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 amino acids
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: circular
                                                   CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                           USA
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                                                                                           COUNTRY:
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                                      ; FEATURE:
, OTHER INFORMATION: Cyclicized modulating agent comprising
, OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1352
                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08520535
Fatent No. 5817750
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
CONNTRY: USA
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Patent No. 595572
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pagqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
                                                                                                                             Score 33; DB 4; Length 10;
Pred. No. 81;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.7%; Score 30; DB 2; Length 8; 80.0%; Pred. No. 3.8e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPAN: (619) 535-9001
TELEFRY: (619) 535-8049
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTER STICS:
LENGTH: 8 amino acids
                                                                                                                               45.8%;
                   ORGANISM: Artificial Sequence
                                                                                                              Ouery Match
Best Local Similarity 60.0
Eaching 6; Conservative
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Best Local Similarity 80.0
Then 4; Conservative
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US-08-520-535-12
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US-08-520-535-12
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US-09-079-432-12
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US-08-986-234-92
US-08-986-234-92
IS-08-986-234-92
Sequence 92, Application US/08986234
Fedenace 92, Application US/08986234
Fedenace 92, Application US/08986234
GENERAL INFORMATION:
APPLICANT: Wallen, et al.
TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
FILE REFERENCE: UNMS-0008-1
CURRENT APPLICATION NUMBER: US/08/986,234
CURRENT FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Datentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,432

FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/520,535

FILING DATE: 28 A-40G-1995

ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-LA 1794

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.7%; Score 30; DB 2; Le
100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
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Sequence 22, Application US/09108709

Patent No. 6008044

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gl
TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gl
TITLE OF INVENTION: Human Monoclonal Antibodies Information of Antibodies Information:

TITLE OF INVENTION: Pusion—associated Epitope (GCSGKLIC) in gp-41

TITLE OF INVENTION: Pusion—associated Epitope (GCSGKLIC) in gp-41

FILE REFERENCE: 10586/00406

CURRENT APPLICATION NUMBER: US/09/108,709

CURRENT FILING DATE: 1998-07-01

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO. 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 110, Application US/09790497A

Sequence 110, Application US/09790497A

Sequence 110, Application US/09790497A

Sequence 110, Application US/09790497A

Sequence 110, Application US/09785

GENERAL INFORMATION:

APPLICANT: De Ley9, Robert

TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT:

TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT:

TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS

TITLE OF INVENTION: CONTAINING THEM

TITLE OF INVENTION: UNMBER: US/09/790,497A

CURRENT FILING DATE: 1996-09-33

PRIOR APPLICATION NUMBER: 09/146,028

PRIOR APPLICATION NUMBER: PCT/EP93/00517

PRIOR APPLICATION NUMBER: PCT/EP93/00517

PRIOR APPLICATION NUMBER: PCT/EP93/00517

PRIOR APPLICATION NUMBER: EP 92400598.6

PRIOR RILING DATE: 1992-03-06

PRIOR PILING DATE: 1992-03-06
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NAME/KEY: PEPTIDE

LOCATION: (1)..(10)

OTHER INFORMATION: amino acids 600-609 according to the Gnann
OTHER INFORMATION: numbering system
US-09-108-709-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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             APPLICANT: Fikes, John D.

APPLICANT: Fikes, John D.

APPLICANT: Batte, Alessandro.

APPLICANT: Ishioka, Gleny G.

APPLICANT: Ishioka, Gleny G.

APPLICANT: Ishioka, Gleny G.

APPLICANT: Livingston, Brian

APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert W.

APPLICANT: Chesnut, Robert W.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an

TITLE OF INVENTION: Emmune Response and Methods of Using the Same

FILE REFERENCE: 39963-2002.01

CURRENT APPLICATION NUMBER: US/09/311,784A

CURRENT APPLICATION NUMBER: US 60/085,751

FRIOR FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSEQ for Windows Version 3.0

FRIOR APPLICATION NUMBER: US 60/085,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 30; DB 4; Length 9; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)
US-09-311-784A-374
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CENERAL INFORMATION:
TITLE OF INVENTION: PROCESS FOR THE DETERMINAT
TITLE OF INVENTION: PROCESS FOR THE DETERMINAT
TITLE OF INVENTION: A PROCESS FOR DETERMINATI
TITLE OF INVENTION: BITTOPES, A PROCESS FOR FILTE OF INVENTION: CONTAINING THEM
FILE OF INVENTION: CONTAINING THEM
FILE REFERENCE: 2752-16
CURRENT APPLICATION NUMBER: US/09/790,497A
CURRENT APPLICATION NUMBER: 09/576,824
PRIOR APPLICATION NUMBER: 09/576,824
PRIOR FILING DATE: 1996-09-30
PRIOR FILING DATE: 1996-09-30
PRIOR PILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR PILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: EP 92400598.6
PRIOR APPLICATION NUMBER: EP 92400598.6
PRIOR PILING DATE: 1993-03-08
NUMBER OF SEQ 1D NOS: 600
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09790497A Patent No. 6649735 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v
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TYPE: amino acid STRANDEDNESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 IWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-530-566-10
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0; Indels
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                                                                                                                                                    US-07-946-237-4

| Sequence 4, Application US/07946237 |
| Sequence 4, Application US/07946237 |
| Patent No. 534887410N: |
| GENERAL INFORMATION: |
| APPLICANT: Savakis, Charalambos |
| APPLICANT: Franz, Gerald H |
| APPLICANT: Loukeris, Athanasios |
| TITLE OF INVENTION: Eukaryotic Transposable Element |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCES: |
| ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. |
| STREET: Two Militia Drive |
| CITY: Lexington |
| STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,237
FILING DATE: 19920914
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DATE: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
RETERENCE/DOCKET NUMBER: BTT92-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1961-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Enkaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 1; Pred. No. 3.8e+05;
0; Mismatches
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US-08-530-566-10
'Sequence 10, Application US/08530566
'Setent No. 5840865
'GENERAL INFORMATION:
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Best Local Similarity 75.0'
4; Conservative
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CITY: Lexington
STATE: Massachusetts
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MOLECULE TYPE: peptide
                                       7 IWGC 10
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VWGC 5
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ZIP: 02173
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ZIP: 02173
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Matches
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COMPUTER READABLE FORM:
                                                                                                                                                       Best Local Similarity 75.0 Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-755-10
           TYPE: amino acid
                                                                                                                                                                                                                         7 IWGC 10
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ORGANISM: Unknown
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                            STRANDEDNESS
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US-08-239-765C-4
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Pred. No. 3.8e+05;
1; Mismatches 0; Indels
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APPLICANT: Franz, Gerald H.
APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Ahenasios
APPLICANT: Linakis, Apostolos G.
TITLE OF INVENTION: Eukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
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MUDIUM TYPE: Floppy disk
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,755
FILING DATE: 27-APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION BOOF
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,542
REGISTRATION NUMBER: 33,542
REGISTRATION NUMBER: 33,542
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEG ID NO: 10:
SEQUENCE CHARACTERISTICS:
INMCTH: 5 amino acids
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REGISTRATION NUMBER: 33,542
TELEPHONE: (781) 861-6240
TELEPHONE: (781) 861-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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Best Local Similarity 75.0'
Matches 3; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
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) OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable ; OTHER INFORMATION: elements US-08-239-765C-4
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RRELINGER, Jeffrey A
HYDE-DERUYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 4; Length 5;
Pred. No. 3.8e+05;
1; Mismatches 0; Indels
40.3%; Score 29; DB 3; Length 5; 75.0%; Pred. No. 3.8e+05;
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                                                                                                                                                                                                                                                                          Sequence 4, Application US/08239765C

Patent No. 646928

GENERAL INFORMATION:
APPLICANT: Savakis, Charalambos
APPLICANT: Franz, Gerald H
APPLICANT: Loukeris, Athanaslos
ITILE OF INVENTION: Bukaryotic Transposable Element
FILE REFERENCE: 18747/1130
CURRENT PILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: 07/946,237
PRIOR APPLICATION NUMBER: 07/946,237
PRIOR APPLICATION NUMBER: 07/946,237
SPRIOR FILING DATE: 1992-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
    ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
    STREET: 624 Ninth Street N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
                                                   1; Mismatches
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GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M
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Query Match
40.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION APPLICATION APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-MR-1998
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-CCT-1997
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-CCT-1996
ATTORNEY/ACENT INFORMATION:
NAME: COOPER, IVer P
REGISTRATION NUMBER: 20,005
REGISTRATION NUMBER: 20,005
TELEFRENCE (202) 628-5197
TELEFRENC CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94
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Search completed: December 30, 2004, 14:44:16 Job time : 24.6667 secs

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Gaps ; 0

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Sequence 34, Application US/10046922; Publication No. US20020164667A1; GENEAL INFORMATION: APPLICANT: Alitalo, Kari; APPLICANT: Koivunen, Erkki
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US-10-046-922-34
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Sequence 34, Appl
Sequence 73, Appl
Sequence 68, Appl
Sequence 1090, Ap
Sequence 1352, Ap
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 69, Appl
Sequence 1454, Appl
Sequence 1454, Appl
Sequence 178, Appl
Sequence 178, Appl
Sequence 178, Appl
                                                                                                                                                                                December 30, 2004, 14:43:15; Search time 81.3333 Seconds (without alignments) 44.229 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-046-922-34
3 US-10-046-922-73
3 US-10-046-922-68
7 US-10-046-922-68
7 US-10-654-578-1090
10S-08-821-739A-90
4 US-10-133-210-69
5 US-10-133-210-69
8 US-10-133-210-69
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 80, Appl
Sequence 185, App
Sequence 104, App
Sequence 374, App
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Sequence 708, App
Sequence 4, Appli
Sequence 154, App
Sequence 8, Appli
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Sequence 1271, Ap
Sequence 154, App
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Sequence 21, Appl
Sequence 10, Appl
                                                              Sequence 80, Ap
Sequence 185, A
Sequence 707, A
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Sequence 305, P
Sequence 792, P
Sequence 793, P
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Sequence 3
Sequence 1
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US-09-832-723-104
US-09-894-018-80
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US-09-894-018-80
US-09-894-018-80
US-10-303-331-104
US-10-311-069-374
US-10-371-069-374
US-10-371-069-374
US-10-474-960A-185
US-10-601-952-707
US-10-474-960A-185
US-10-601-953-48
US-10-132-266-708
US-09-913-210-8
US-10-131-210-8
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US-10-371-645-348
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US-10-371-665-348
US-10-371-659-348
US-10-371-260-348
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US-09-947-925A-21
US-10-094-401-10
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US-10-046-922-35

Sequence 35, Application US/10046922

Sequence 35, Application No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kolvunen, Erkki

APPLICANT: Kolvunen, Erkki

APPLICANT: Kolvunen, Erkki

PAPLICANT: Kolvunen, Erkki

APPLICANT: Wolvunen, Erkki

PAPLICANT: Wolver-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVERTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVERTION NUMBER: US/10/046,922

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT APPLICATION VOMBER: US/10/046,922

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 35 100.0%; Score 72; DB 13; Length 10; 100.0%; Pred. No. 0.0026; Indels 0; Mismatches ; ORGANISM: isolated peptide US-10-046-922-35 Best Local Similarity 100. Matches 10; Conservative

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US-10-046-922-68

Sequence 68, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Erki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGRE-3 INHIBITOR MATERIALS AND METHODS
TITLE OF INVENTION: VEGRE-3 INHIBITOR MATERIALS AND METHODS
TITLE OF INVENTION: VEGRE-3 INHIBITOR MATERIALS AND METHODS
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 28967/37084A
CURRENT PEPLICATION VUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 67
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C10
CURRENT APPLICATION NUMBER: US/10/654,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.8%; Score 33; DB 13; Length 8; 57.1%; Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                    ; IOCATION: (4)..(6); OTHER INFORMATION: X at position 4-6 is any amino acid US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                             h Similarity 57.1%; Pred. No. 1.5e+06; 4; Conservative 0; Mismatches 3
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NAWE/KEY: SITE
COCATION: (4)...(6)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (8)...(8)
OTHER INFORMATION: X is any amino acid
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US-10-654-578-1090
S-20-654-578-1090
Sequence 1090, Application US/10654578
Publication No. US20040229811A1
GENERAL INFORMATION:
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                      TYPE: PRT
ORGANISM: peptide
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ORGANISM: peptide
                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
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US-10-046-922-73
Sequence 73, Application US/10046922
Sequence 73, Application US/10046922
Sequence 73, Application Wo. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kolovnen, Erki
APPLICANT: Kolovnen, Erki
APPLICANT: Robo, Hajime
TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
CURRENT APPLICATION UNDER: 28097/37084A
CURRENT FILING DATE: 2002-01-15
VUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 73
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.72; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Score 50; DB 13; Length 10; 60.0%; Pred. No. 2.5; tive 0; Mismatches 4; Indels
           APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGRR-3 INHIBITOR MATERIALS AND METHODS
FILE REPERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT APPLING DATE: 2002-01-15
WUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
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; OTHER INFORMATION: X is any amino acid
US-10-046-922-34
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LOCATION: (9)...(9)

COTHER INFORMATION: X is any amino acid
US-10-046-922-73
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OTHER INFORMATION: X is any amino acid
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Publication No. US20020164667A1
GENERAL INFORMATION:
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
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APPLICANT: Kubo, Hajime
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Best Local Similarity 100.
Matches 8; Conservative
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APPLICANT: Koivunen, Br)
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NAME/KEY: SITE
LOCATION: (1)...
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NAME/KEY: SITE
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US-10-046-922-67
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LENGTH: 10
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PRIOR APPLICATION NUMBER: 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR PILING DATE: 1994-12-01
PRIOR PILING DATE: 1994-01-25
PRIOR APPLICATION NUMBER: 08/159,339
PRIOR APPLICATION NUMBER: 08/159,339
PRIOR PILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: 08/027,746
PRIOR APPLICATION NUMBER: 08/027,746
PRIOR PILING DATE: 1993-03-05
PRIOR PILING DATE: 1993-03-05
PRIOR PILING DATE: 1993-08-07
PRIOR PILING DATE: 1992-08-07
NUMBER OF SEQ 1D NOS: 149
NUMBER OF SEQ 1D NOS: 149
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FUBLICATION NO. US20030103964A1
APPLICANT: DeLigi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakar
APPLICANT: Vaccaro, Dennis
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-08-821-739A-90
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Best Local Similarity
Matches 5; Conserv
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2 LGIWGC 7
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OTHER INFORMATION: Cyclicized modulating agent comprising
OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1352
                                                                                                                                                                                                             OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence US-10-654-578-1090
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| Sequence 1352, Application US/10654578
| Publication No. US20040229811A1
| GENERAL INFORMATION:
| APPLICANT: Blachuk, Orest W. APPLICANT: Symonds, James Matthew
| APPLICANT: Gymonds, James Matthew
| TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
| TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
| CURRENT APPLICATION NUMBER: US/10/654,578
| CURRENT FILING DATE: 2003-09-03
| NUMBER OF SEQ ID NOS: 2009
| SEQ ID NO 1352
| LENGTH: 10
                                                                                                                                                                                                                                                                                                                         Query Match 45.8%; Score 33; DB 17; Length 10; Best Local Similarity 60.0%; Pred. No. 5e+02; Matches 6; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels
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APPLICANT: Kubo, Ralph T.
APPLICANT: Gray, Howard M.
APPLICANT: Gray, Howard M.
APPLICANT: Gray, Howard M.
APPLICANT: Gette, Alessandro
APPLICANT: Gette, Beteban
ITTLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060-005000A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT APPLICATION NUMBER: G0/013,833
PRIOR APPLICATION NUMBER: 08/589,107
PRIOR APPLICATION NUMBER: 08/589,107
PRIOR APPLICATION NUMBER: 08/519,107
PRIOR APPLICATION NUMBER: 08/51,913
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1090
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGYWLTIWGC 10
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                                                      Gape
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APPLICANT: Delisi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakar
APPLICANT: Vaccaro, Dennis
APPLICANT: Vaccaro, Dennis
APPLICANT: Weng, Zhiping
APPLICANT: Weng, Zhiping
APPLICANT: Weng, Chiping
APPLICANT: Chang, Chap
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REFERENCE: BU-035-04-26
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
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83.3%; Pred. No. 6.8e+02;
ative 0; Mismatches 1; Indels
Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:
US-10-133-210-39
  Score 32; DB 8;
Pred. No. 6.8e+02;
                                                   0; Mismatches
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Gaps
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                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                               APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060.005,000A,
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1999-03-20
FRIOR PILING DATE: 1996-03-21
PRIOR PLLING DATE: 1996-03-21
PRIOR APPLICATION NUMBER: 08/589,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%; Score 30; DB 8; Length 9; 100.0%; Pred. No. 1.5e+06;
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US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US2002098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
                                                               Score 31; DB 10;
Pred. No. 9.3e+02;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 78, Application US/08821739A Publication No. US20020168374A1
     ; OTHER INFORMATION: in this patent. US-09-572-404B-1454
                                                                 Query Match 43.1
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                            2 GYWLTIWG 9
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Best Local Similarity
Matches 4; Conserv
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OTHER INFORMATION: sequence located in P2RYS at 139-148 and may interact with Sequen
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; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
    APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFRENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
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APPLICANT: Weng, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
TILE REFERENCE: 10-035AX
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 69
LENGTH: 10
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-133-210-69
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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION UNMERR: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                     44.4%; Score 32; DB 14; Length 10; 83.3%; Pred. No. 6.8e+02;
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Pred. No. 1.5e+06;
0; Mismatches 3; Indels
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57.1%;
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Best Local Similarity 83.5.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-046-922-36
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PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104
TYPE: PRI
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptides screened from a phage display random US-09-832-723-104
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41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                     Query Match .41.7%; Score 30; DB 9; Length 9; Best Local Similarity 50.0%; Pred. No. 1.5e+06; Matches 4; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Sequence 80, Application US/09894018

j. Sequence 80, Application US/09894018

j. Patent No. US20020119127A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Chestnut, Robert

APPLICANT: Baker, Denisw

APPLICANT: Newman, Mark

APPLICANT: Scoun, Brian

APPLICANT: Newman, Mark

APPLICANT: Newman, Mark

APPLICANT: Newman, Mark

APPLICANT: NUMBER: 10509/894,018

CURRENT APPLICATION NUMBER: CO1-6-27

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEC ID NOS: 368

SOFTWARE: FASTERE for Windows Version 4.0

FEWALTION OF SEC ID NOS: 368
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COTHER INFORMATION: Oligopeptide
US-09-894-018-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGYWLTIW 8
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US-09-894-018-80
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Search completed: December 30, 2004, 15:04:06 Job time : 81.3333 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
           Copyright
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- protein search, using sw model OM protein December 30, 2004, 14:30:43; Search time 18.6667 Seconds (without alignments) 51.545 Million cell updates/sec Run on:

US-10-046-922-35 72 Title: Perfect score:

1 CGYWLTIWGC 10 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 MaximummDBmseqmlengthmm.o.r.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query. Match	Length	BB	ID	Description
-1	24	33.3	10	. ~	S71868	glutathione transf
~	24	33.3	10	7	A35556	hypothetical prote
m	22	30.6	7	7	PT0586	u
4	22	30.6	10	7	T17075	
ស	21	29.5	10	~	E41946	T-cell receptor qa
9	20	27.8	S	N	JH0253	pentapeptide
7	20	27.8	9	N	F41946	T-cell receptor qa
80	20	27.8	80	~	S19288	acylase - Kluyvera
ი	19	26.4	0	N	PT0324	Ig heavy chain CRD
10	19	26.4	10	ď	PT0289	
11	19	26.4	10	7	E49033	
12	19	26.4	10	0	F49033	
13	19	26.4	10	~	C41946	
14	18	25.0	80	N	JS0315	leucokinin V - Mad
. 15	18	25.0	10	N	PT0230	Ig heavy chain CDR
16	18	25.0	10	~	PH0923	T-cell receptor be
17	18	25.0	10	N	F33932	Ig mu chain J regi
18	18	25.0	10	4	S14943	UGA3 leader peptid
19	17	23.6	4	~	B53284	recep
20	17	23.6	9	0	PT0629	
21	17		9	N	PT0637	T-cell receptor be
22	17	23.6	9	~	A61068	locustakinin - mig
23	17	23.6	9	4	179564	hypothetical TCL3
24	17	23.6	7	~	PT0628	T-cell receptor be
25	17	23.6	7	N	PT0642	
56	17	23.6	7	N	PT0722	T-cell receptor be
27	17	23.6	7	7	PT0728	T-cell receptor be
28	17	23.6	7	~	PX0008	~
59	17	23.6	7	~	B48394	major fat-globule

hypothetical protein (ODC region) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: A35556 R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D. J. Biol. Chem. 265, 4884-4892, 1990 A;Title: Isolation and expression of a human ornithine decarboxylase gene. A;Reference number: A35556; MUID:90202959; PMID:2318872

A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA

A; Cross-references: GB:J05271

Query Match

33.3%; Score 24; DB 2; Length 10;

pev-kinin 1 - pena	triacylglycerol li	neuromodulatory pe	neuromodulatory pe	neuromodulatory pe	T-cell receptor be	leucokinin VI - Ma	leucokinin VII - M	leucokinin VIII -	angiotensin-conver	adipokinetic hormo	T-cell receptor be	T-cell receptor be	sperm-activating p	hypotrehalosemic h	hypertrehalosemic
PD0029	S57274	S33244	S33245	S33246	PT0724	JS0316	JS0317	JS0318	A31570	A24244	PT0634	PT0562	A60522	B33995	208997
7	7	~	N	~	~	~	~	0	~	~	~	~	~	~	0
7	7	7	7	7	œ	α	60	80	6 0	თ	δ	σ	σ	10	10
23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6
17	17	17	17	17	17	17	17	17	17	11	17	17	17	17	17
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sylason
glutathione transferase (BC 2.5.1.18) class mu 4 - pig (fragment)
NyAlternate names: glutathione S-transferase class mu 4
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: S71868
B;Ochem. J 317, Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J 317, 879-884, 1996
A;Aitle: Characterization of pig liver glutathione S-transferases using HPLC-electrospra
A;Reference number: S71864; MUID:96332484; PMID:8760377
                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-10 <ROU>
C;Comment: At least five species-independent classes of cytosolic glutathion transferasc c;Complex: dimer
C;Complex: dimer
C;Complex: dimer
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a A, Pathway: detoxification; xenobiotics metabolism
A, Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              es of damage
C;Superfamily: glutathione transferase
C;Keywords: dimer; transferase
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Best Local Similarity
Matches 3; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GYW 4
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A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastr;
, and of the circular muscle of the gastro-intestinal junction.
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R;Wheteell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger
A;Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CiSpecies: Kluyvera cryocrescens
CiDate: 19-War-1997 #sequence_revision 19-War-1997 #text_change 09-Jul-2004
CiAccession: S19288
RiMartin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                             gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar_1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
                                                                                                                                                                                                                Gaps
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                             not compared with conceptual translation
                                                                                                                                                          Length 10;
                                                                                                                                                        Score 21; DB 2; Length 10;
Pred. No. 2.8e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 2; Length 6;
Pred. No. 2.8e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5;
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66.7%; Pred. No. 2.8e+05;
iive 1; Mismatches 0;
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                                                                                                                                                          Query Match 29.2
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity 40.0
Matches 2; Conservative
A,Accession: E41946
A,Status: preliminary; not C
A,Molecule type: DNA
A,Residues: 1-10 <WHE>
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-5 <UES>
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Best Local Similarity
Matches 2; Conserv
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1 GFW 3
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C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Accession: E41946 # Since Sequence analyses of F.V.; Miller, K.S.; Klein, J.R. R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. A; Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge A; Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Species: mitochondrion Chamaeleo fischeri
C;Species: mitochondrion Chamaeleo fischeri
C;Species: mitochondrion Chamaeleo fischeri
C;Species: mitochondrion
I:0.04
C;Accession: T1075
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A;Reference number: Z18674; MUID:97315309; PMID:9169559
                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Paccession: PT0586; PT0592
C;Paccession: PT0586; PT0599; MUID:91277601; PMID:1711558
A;Paccession: PT0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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75.0%; Pred. No. 2.8e+05;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor gamma chain (1a.9) - mouse (fragment)
        Pred. No. 9.9e+02;
0; Mismatches 1
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Pred. No. 2e+03;
0; Mismatches
                                                                                                                                                                                                                                                                T-cell receptor beta chain V-D-J region (141-1CN)
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A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.6%;
  75.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
Similarity 75.03; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA A; Residues: 1-7 <FEE>
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3 SIWG 6
                                                                                  1 CGYW 4
                                                                                                                                  CGAW 8
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        Best Local
Matches
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2; Indels

Length 10;

DB 2; I 5.4e+03;

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T-cell receptor gamma chain (1t.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C4194 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma shacerence number: A41946; MUID:92049316; PMID:1658619
A;Accession: C41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
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C;Species: Homo sapiens (man)
C;Species: 19-Dec-1933 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F49033 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
E;Accession: F49033 #sequence_revision P: Martinez, C:; Spits, H:; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Punctionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
                                   R,Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B. Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Punctionally distinct subsets of human gamma/delta T cells.
A;Fitle: Runctionally MIDI:92083926; PMID:1684157
                                                                                                                                                                                                                                                                 A;Molecule type: DNA,
Mseaidues: 1-10 AMOR-
A;Kesidues: 1-10 AMOR-
A;Cross-references: GB:S72587; NID:gZ40696; PIDN:AAB20630.1; PID:gZ40697
A;Cross-reference extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 MONE2>
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A;Cross-reference extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)
C;Keywords: T-cell receptor
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A;ReBidues: 1-10 AMOR>
A;Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701
A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)
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50.0%; Pred. No. 5.4e+03;
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Pred. No. 5.4e+
0; Mismatches
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Best Local Similarity 50.00,
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                               A; Accession: E49033
A; Status: preliminary
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: All Species: All Species
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: PT0289
R;Yamada, M: Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
T. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Accession: PT0289
A;Accession: PT0289
A;Accession: PT0289
A;Aseidues: I-10 < YAM>
A;Resperimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from A;Title: Chemical modification of serine at the active site of penicillin acylase from A;Reference number: 519288; MUID:92109664; PMID:1764029
A;Rocession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule acklass
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B49033
T-cell receptor gamma chain V-D-J region - human (fragment).
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
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Pred. No. 5.4e+03;
3; Mismatches 1; Indels
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33.3%;
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C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: O'7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic A;Reference number: JS0315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P19987
A;Comment: Leucokining, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
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Global Sepident (clone 1-118A) - human (fragment)
Cjgheavy chain CDR3 region (clone 1-118A) - human (fragment)
Cjgheceis: Homo sapiens (man)
Cjbate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
Cjbate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
SjAccesion: PR0230
B;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Pitle: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Accession: PT0230
A;Molecule type: DNA
A;Residues: 110 cYAM>
A;Residues: 110 cYAM>
A;Residues: 110 cYAM>
A;Residues: heterotetramer; immunoglobulin
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2; Indels
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leucokinin V - Madeira cockroach
2; Conservative
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A, Molecule type: protein
A, Residues: 1-8 <HOL>
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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QBSHF6
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Maximum Match 100%
Listing first 45 summaries
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CAD45547
CAD45847
Q85HN1
Q6JL97
AAS16521
Q85DB0
Q94NA9
Q94NB1
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Q98SHG6
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Gapop 10.0 , Gapext 0.5
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	ALIGNMENTS	10 AA.	update) on update)	. nut). Streptophyta; Embryophyta; T ta; eudicotyledons; core eud Euphorbiaceae; Crotonoideae;	(1) TISSUE-Latex; TISSUE-Latex; Kosssi S., van der Sluis W.G., Boelens R., T'Hart L Labaditin, a novel cyclic decapeptide from the late: multifida L. (Euphorbiaceae). Isolation and sequence	9 C S E	wounds, skins infe D98AAD6362D1B362 CR	re 30.5; DB 1; id. No. 5.4e+02; Mismatches 1;		0
Q8SHE7 Q8SHF3 Q8SHGF9 Q8SHG6 Q8SHH1 Q8SHH4 Q8SHH4 Q8SH10 Q8SH13 Q8SH13 Q8SH19 Q8SH19 Q8SH19	ALIG	PRT;	Created) Last sequence up Last annotation	nut). itreptoph :a, eudic :uphorbia	G., Boel decapept). Isola R.";	an activ mplement interac eptide. this pl	ed wound D98AAD	Score 30. Pred. No. 1; Mismat		P Cre Las Las t I cha
000000000000000			eat at at	ic , S hyt , E	Back.	g; is cp	Mar.	4 8 ;		21, 21, 25, uni uni r's dat
		STANDARD;	13, 13, 44,	Labaditin. Jatropha multifida (Physic nut Eukaryota, Viridiplantaa, Stre Spermatophyta; Magnoliophyta; eurosids I; Malpighiales; Euph Jatropha. NCBL_TaxID=3996;	r Sluis el cycl horbiac	aditin hway of ased on a cyclic	atment of infecting.	42 62 /ativ	6 8	INARY; Lrel. Lrel. Lrel. Lrel. Grel.
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ოოოოოოოოოოოო				ult Vi yta , M	ex; <a, <a<="" td=""><td>25 DN: Cal</td><td>eat 10</td><td>ni 1</td><td>GYWL GVW-</td><td>Pi (() () () () () () () () ()</td></a,>	25 DN: Cal	eat 10	ni 1	GYWL GVW-	Pi (() () () () () () () () ()
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Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoldeae; Ocimeae; Fuerstia.
                                                                                                                                                               Paron A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL: AJ505427; CAD45547.1; -...
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"Characterization of pig liver glutathione S-transferases using HPLC-electrospraty-ionization masses spectrometry.";
Biochem. J. 317:879-884 (1996).
PIR: $71868; $71868.
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1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
01-MAR-2004 (TrEMBLrel. 26, Last annocation update)
Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
Sus scrofe domestica (domestic pig).
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          8 AA; 916 MW; DABEAB58637041B5 CRC64;
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Matches 3; Conservative
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               Fuerstia africana.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL, AJ50427; CAD45547.1; -...
GO; GO:0003735; F:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                     Townsend T., Larson A.; "Molecular phylogenetics and mitochondrial genomic evolution in the "molecular phylogenetics, Squamata)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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                                                                                                                                                                   Townsend T.M., Larson A.L.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF444875, AAL90547.1; -
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                   5E218E2733772727 CRC64;
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14-MAR-2004 (TrEMBLrel. 27, Created)
14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Ribosomal protein (Fragment).
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Last annotation update)
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                 SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
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10 AA; 1276 MW;
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05-JUL-2004 (TrEMBLrel. 27,
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WLLLW 6
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SEQUENCE FROM N.A.
MEDLINE-22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                         STRAIN=MS11;
PubMed=15084227;
Snyder L.A., Davies J.K., Saunders N.J.;
Microarray genomotyping of key experimental strains of Neisseria gonorrhoeae reveals gene complement diversity and five new neisserial genes associated with Minimal Mobile Elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
NCBI_TaxID=78584;
                                                                                  Neisseria gonorrhoeae.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Snyder L.A.S., Davies J.K., Saunders N.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 10 AA; 1227 MW; BACCBB286379D1A6 CRC64;
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NON TER 1 1 SEQUENCE 9 AA, 1174 MW, 16C563636B5045B0 CRC64;
 20-MAY-2004 (TrEMBLrel. 27, Created)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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EMBL; AF224597; AAP33652.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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Matches 3; Conserv
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Matches 4: Conserv
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                                                    Nuol (Fragment).
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"Microarray genomocyping of key experimental strains of Neisseria gonorrhoeae reveals gene complement diversity and five new neisserial genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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                                                                                                                 "Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
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Barteria, proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
NCBI_TaxID=485,
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
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Pred. No. 4.8e+03;
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF4448730; AAL90472.1;
GO; GO:0005739; C:mitochondrion; IEA.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, #X186266; AAS16521.1; -.
                                                                                                                                                                                                                                                                          Mitochondrion.
NON TER 10 10
SEQUENCE 10 AA; 1327 MW, 5E2180C7336415B7 CRC64;
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MEDLINE=22169767; PubMed=12182400;
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                  Bradypodion.
NCBI_TaxID=179888;
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2 WLSRW 6
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AAS16521;
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MEDINE-22631663; PubMed-12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M. Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                               Score 23.5; DB 2; Length 9;
Pred. No. 1.8e+06;
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                                                                       D5C563636B5045A2 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last annotati
Cytochrome oxidase subunit III (Fragment)
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EMBL, AF224637, AAK70599.1; --
EMBL, AF224639; AAK70603.1; --
EMBL, AF224639; AAK70607.1; --
GO, GO.0005739; C.mitochondrion; IEA.
Mitochondrion. 1
SEQUENCE 9 AA, 1160 MW; D5C563636B5
  GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NON TER 1
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01-DEC-2001 (TrEMBLrel. 19, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microcebus rufus (Brown mouse lemur)
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                                                                                                               32.6%;
57.1%;
                                                                  SEQUENCE 9 AA; 1160 MW;
                                                                                                                                                                 4; Conservative
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                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=122232;
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Q94NB0
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Q94NB1
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Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIJINE=22831663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy"."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=22281620; PubMed=12393004;
Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence from
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
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Mammalia; Eutheria; Primates; Strepsirhini; Daubentoniidae;
Daubentonia.
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
Name=COIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
                                                                                                                                                                                  Lepilemur edwardsi (Milne-Edwards's sportive lemur) Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
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EMBL; AF224641; AAK70615.1; -.
EMBL; AF224642; AAK70619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
EMBL; AF224595; AAP33644.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum. Evol. 43:463-478(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.6%;
57.1%;
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                          PRELIMINARY;
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AC 0083
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MEDLINE=21184272; PubMed=11286490;
MEDLINE=21184272; PubMed=11286490;
Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemuly family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R., "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences "; Mol. Phylogenet. Evol. 19:45-56 (2001).
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Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Strepsirhini; Cheirogaleidae;
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Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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Pred. No. 1.8e+06;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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9 AA; 1160 MW; D5C563636B5045A2 CRC64;
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EMBL; AF224624; AAK70547.1; -.
EMBL; AF224625; AAK70551.1; -.
EMBL; AF224627; AAK70551.1; -.
EMBL; AF224627; AAK70559.1. -.
                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
EMBL, AF224630; AAXVO571.1; -.
EMBL, AF224631; AAXVO575.1; -.
GO: GO:0005739; C:mitochondrion; IEA.
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Name=COIII;
Microcebus murinus (Lesser mouse lemur).
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GO; GO:0005739; C:mitochondrion; IEA.
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57.1%;
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Best Local Similarity
Matches 4; Conserv
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                                               NCBI_TaxID=122231;
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NON TER 1
SEQUENCE 9 AA.
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Mammalia;
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SEQUENCE
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MEDLINE=21396409; PubMed=11504862;
Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
"Increased-rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects.";
Mol. Biol. Evol. 18:1828-1832(2001).
EMBL, AF335990; AAK52583.1; -..
GO, GO:005739; C:mitochondrion; IEA.
                                                  Gaps
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Neoptera, Paraneoptera, Hemiptera, Buhemiptera, Heteroptera,
Panheteroptera, Pentatomomorpha, Pentatomoidea, Pentatomidae,
    Length 9;
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Pred. No. 1.8e+06;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome c oxidase subunit III (Fragment).
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Score 23.5; DB 2;
Pred. No. 1.8e+06;
0; Mismatches 0;
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Best Local Similarity
Matches 4; Conser
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                                                                                              3 YWLTIWG
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5.1.6 Compugen Ltd GenCore version (c) 1993 - 2005 Copyright

- protein search, using sw model OM protein

Run on:

January 3, 2005, 11:51:33 ; Search time 150 Seconds (without alignments) 19.132 Million cell updates/sec

SE032 score: Title: Perfect (

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003ss:* geneseqp2003bs:* A_Geneseq_23Sep04: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		'R-3 b	7R-3 b	Fc region	Human ser	Protein e	faeciu	Human HIV	Human ATP	Mouse ATP	A human M	in ATP	Homo sapi	Fc region	ın ser	Peptide #	Peptide #	noq u								
	ion	VEGFR-	VEGFR-3				Ю.					. Human	Human	Human	Human		Human	. Human	Human	Homc		Human				
	Description	Abp53931	Abp53932	Aao26093	Adj50760	Abu30004	Adc97318	Aab62747	Aae09365	Aae09362	Aay43544	Aae09361	Aae09370	Aae09367	Aae09368	Aae09369	Aae09364	Aae09371	Aae09363	Abp52113	Aao26134	Adj50801	Abb38460	Aam31901	Aam71604	
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OUTWAKIES		11	7	23	0.0	14	80	7	5	22	4		0		8	6.	4	7		ь.	4	11	0	1	4	
SOM	QI	ABP53931	ABP53932	AA026093	ADJ50760	ABU30004	ADC97318	AAB62747	AAE09365	AAE09362	AAY43544	AAE09361	AAE0937	AAE09367	AAE09368	AAE09369	AAE09364	AAE0937	AAE0936.	ABP5211	AA026134	ADJ50803	ABB38460	AAM31901	AAM71604	
	DB	20	S	9	σ,	9	7	4	4	4	0	4	4	4	4	4	4	4	4	S	9	œ	4	4	4	
	Length	10	10	13	13	474	492	120	1140	1498	1503	1503	1503	1503	1503	1503	1503	1503	1503	1503	14	14	34	34	34	
de	Query	100.0	100.0	79.6	79.6	79.6	9.64	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	75.9	75.9	75.9	75.9	75.9	
	Score	54	54	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	41	41	41	41	41	
	Result No.		2	e	4	2	9	7	80	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Abg51286 Human liv Abg41416 Human pep Aay00213 Enterococo Abb43432 E faecali Abu188460 E. faecali Abu18711 Enterococo Adh87431 E faecali Abu18745 Enterococo Aby8431 E faecali Abu13710 Enterococo Aby86452 Fibermocococo Adh6127 Fibermocococococococococococococococococococ	
ABG53286 ABG41416 AAY00213 AAY00213 ABU88460 ABU88460 AAY00212 AAY00212 AAY00212 AAY00212 AAY00212 ABG7261 ABG7261 AAG727269 ABG77269 ABG77269 ABG77263	
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# ALIGNMENTS

RESULT 1 ABP5393

ABP53931 standard; peptide; 10 AA.

ABP53931;

(first entry) 09-JAN-2003

VEGFR-3 binding peptide SEQ ID NO:34.

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. 

Ното варіепв. Synthetic.

Location/Qualifiers Misc-difference 1

/note= "any amino acid" 'note= "any amino acid" Misc-difference 10

WO200257299-A2

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

17-JAN-2001; 2001US-0262476P.

(LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.

Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 12; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

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                              have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, brasst, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangloms and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated peptide (1) that binds to and inhibits vascular endothelial growth factor receptor 3 (VBCRR-3). (1) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and texting disorders mediated by the activity of the cell surface receptor VBGRR-3 such as cancer, e.g. brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; heparotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Score 54; DB 5; Length 10; Similarity 100.0%; Pred. No. 0.091; 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGFR-3 binding peptide SEQ ID NO:35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-691521/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 AA;
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liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. Hypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Pc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. whole blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides, useful as binding molecules for detecting, isolating purifying immunoglobulin Fc-region polypeptides present in a solution, for regulating or preventing an antibody response.
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Pred. No. 5.2;
1; Mismatches 2; Indels
                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                  100.0%; Score 54; DB 5;
100.0%; Pred. No. 0.091;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fc region binding peptide SEQ ID No 73.
                                                                                                                                                                                                                                                                                                                                                   AAO26093 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002; 2002WO-US012492.
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                                                                                                                                                                                Local Similarity
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                                                                                                                                      Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                  AA026093;
                                                                                                                                                                  Query Match
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GYWCNVWG

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human serum albumin; HSA; serum; blood; tumour; human.
                                                       Human serum albumin binding peptide, Seq ID No 297.
                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 297; 191pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU30004 standard; protein; 474 AA.
            ADJ50760 standard; peptide; 13 AA
                                                                                                                             16-JUN-2003; 2003WO-US018896
                                                                                                                                           14-JUN-2002; 2002US-0388642P
                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                  Similarity 62.9
5; Conservative
                                                                                                                                                                                                                                                                                                                                                method of the invention
                                                                                                                                                                        Dawson BM;
                                                                                                                                                                                      WPI; 2004-082161/08
                                                                                                                                                                                                                                                                                                                                                                                                        GYWLTIWG 8
                                                                                                                                                         (DYAX-) DYAX CORP.
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                                                                                                 WO2003106493-A1.
                                                                                                                                                                                                                                                                                                                                                             Sequence 13 AA;
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                                                                                   Homo sapiens.
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                                         06-MAY-2004
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                                                                                                                                                                        Sato AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU30004;
                           ADJ50760;
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Best Local &
RESULT 4
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       ADJ50760
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                                                                                                                                                                                                                                                                                                                          The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that specifically binds to (I), allowing the (I)-binding agent to bind to (I) to form a complex including one or more compounds physically associated with (I), separating the complex from one or more compounds of the compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the
Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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79.6%; Score 43; DB 8; Length 13; 62.5%; Pred. No. 5.2; ive 1; Mismatches 2; Indels
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Protein encoded by Prokaryotic essential gene #15531.

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Indels

1,

79.6%; Score 43; DB 6; I 85.7%; Pred. No. 1.8e+02; ive 0; Mismatches 1;

Conservative

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Best Loc Matches

Local Similarity

Query Match

GYWLTCW 100

1 GYWLTIW 7

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Length 474;

The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a product operably linked to the nucleic acid nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a product operably linked to the nucleic acid conceding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation or the activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-cequired gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for collection of a collection of a constraint or solds are useful for a for all and all and actions or a dentifying proteins or screening for homologous nucleic acids are useful for a for a dentifying proteins. New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH: Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Claim 25; SEQ ID NO 57928; 1766pp; English. ftp.wipo.int/pub/published_pct_sequences Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 (ELIT-) ELITRA PHARM INC Enterococcus faecium. Zamudio C, Trawick JD, 2003-029926/02 N-PSDB; ACA33874 Sequence 474 AA; WO200277183-A2 03-OCT-2002 oʻr Wang | 

Page

ADC97318;

RESULT 6 ADC97318

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The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gpl20, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
                                                                                                                          Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
envelope glycoprotein; gpl20; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%; Score 42; DB 4; Length 120; 62.5%; Pred. No. 65;
                                                                                     Human HIV-1 monoclonal antibody SEQ ID NO: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 51-52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-US017327.
                                         (first entry)
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Best Local Similarity 62.5
Pest Local Similarity 52.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watkins BA, Reitz MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 GYWVSYWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112438/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYWLTIWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 120 AA;
                                                                                                                                                                                                                                             WO200100678-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant; mutein
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1999;
                                           03-APR-2001
                                                                                                                                                                                                                                                                                       04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
AAB62747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE09365
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid derived from
Enterococcus faecium encoding an Enterococcus faecium polypeptide having
one of 10 fully defined sequences given in the for comprising 40
complement or leader chosen from any of the nucleic acids, its
complement or sequences hybridish to it). Also included are a
recombinant vector comprising the nucleic acid operably linked to
transcription regulatory element, a cell comprising the vector and a
single-stranded probe comprising the nucleic acid. The nucleic acids are
chosen from 364 disclosed sequences encoding 3654 disclosed proteins.
The nucleic acids is useful for diagnosing pathological conditions
resulting from E. faecium bacterial infection (e.g. urinary tract
infection) and for screening drugs such as agonists and antagonists. The
nucleic acid is useful for recombinant production of Candida albicans
cuffection) and for screening drugs such as agonists and antagonists.
Conflict acid is useful for recombinant production of Candida albicans
curletication between the nucleic acid are useful for preventing or
treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                        Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 43; DB 7; Length 492
85.7%; Pred. No. 1.8e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 6945; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            one if the disclosed E. faecium proteins
                                                                                                                                                                                                 E. faecium protein sequence SEQ ID 6945.
                                                                ADC97318 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00107532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doucette-Stamm LA, Bush D;
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                              Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYWLTCW 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWLTIW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                         US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1998;
                                                                                                                                                        01-JAN-2004
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Gaps

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Indels

23-FEB-2001; 2001WO-US005741.

30-AUG-2001.

AAB62747 standard; protein; 120 AA.

RESULT 7
AAB62747
ID AAB6

112

Query Match

30-AUG-2001.

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a C Mysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-composure on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane domains PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for counselling in the area of genetic testing, carrier detection and prenatal delagnosis. The present sequence is human ATP-binding cassette (ABC) transporter. ABCC6 (MRP6) truncated mutant which is obtained as the result of a stop codon at position little MRP6 protein. Note: The human are all areas and the transporter and the present expense transporter as accounted transporter at a page of the px and a page of the px and a page of the px area to the human and prenatal contents and the human area and the present esquence is human and prenately and the present esquence is human and prenately for result of a stop codon at position little of the protein of stop in the present at the present and the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in figure 3 of the specification (AAE09361)
                                                                                                                                                                                                                                                                                                                          Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                   Terry S;
                                                                                                                                                                            Urban Z,
                                                                                                                                                                            Lesaux O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page; 163pp; English
                            23-FEB-2000; 2000US-0184269P.
                                                                                                                                                                            Boyd CD, Csiszar K,
                                                                                                                                                                                                                                        2001-536645/59.
                                                                                    PXE INT INC
UNIV HAWAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1140 AA;
                                                                                                                                                                                                                                                                        N-PSDB; AAD16258
                                                                                    (PXEI-)
                                                                                                                       (UYHA-)
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77.8%; Score 42; DB 4; Length 1140; 71.4%; Pred. No. 5.9e+02; ive 2; Mismatches 0; Indels Query Match Best Local Similarity 71.4 Marches 5; Conservative 1 GYWLTIW 7 ద ઠ

965 GYWLSLW 971

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Gaps ö

> AAE09362 standard; protein; 1498 AA. (first entry) 19-NOV-2001 AAE09362;

Mouse ATP-binding cassette transporter ABCC6 (MRP6) protein.

Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorthage.

Mus musculus

WO200162977-A2

Location/Qualifiers

Misc-difference 1215

Homo sapiens

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding of the passence of a passence of a passence of a protein located in the plasma membrane containing 17 membrane spanning content in located in the plasma membrane containing 17 membrane and sin autosomal recessive phenotype or appears as a sporadic phenotype. PXE is autosomal recessive phenotype or appears as a sporadic phenotype. PXE is autosomal recessive phenotype or appears as a sporadic phenotype. PXE is associated laxity and loss of elasticity, arterial insufficiency, associated MRP6 alleles who are then provided with appropriate genetic individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic connscilling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal carriers. ABCC6 (MRP6) protein belonging to sub-family "C". Since Resistance associated protein 6 (MRP6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                        identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                                                                                        Screening presence of Pseudoxanthoma elasticum mutation useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.8%; Score 42; DB 4; Length 1498; 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, MPR-related ABC transporter; MOAT protein; MOAT-E; MOAT mediated transport; anticancer drug sensitivity; transporter mediated cellular efflux; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human MPR-related ABC transporter designated MOAT-E.
                                                                                                                                                                          ŝ
                                                                                                                                                                        Terry
                                                                                                                                                                          Urban Z,
                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 152-159; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY43544 standard; protein; 1503 AA.
                                                                                                                                                                          Lesaux O,
                                    23-FEB-2001; 2001WO-US005741.
                                                                         23-FEB-2000; 2000US-0184269P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2000 (first entry)
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                                                                                                                                                                        Ceiszar K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990 GYWLSLW 966
                                                                                                                                                                                                               WPI; 2001-536645/59.
                                                                                                                                  (UYHA-) UNIV HAWAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                 N-PSDB; AAD16236
                                                                                                               (PXEI-) PXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY43544;
                                                                                                                                                                          Boyd CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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0x2x5x8x5x8x5t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resisterace-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; pseudoxanthoma elasticum; PRE; heritable disorder; retinal haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/note= "Nucleotide binding fold-1 (NFB-1) region"
747. .768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transporter gene useful for screening for anti-cancer drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.8%; Score 42; DB 2; Length 1503; 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Indels
"encoded by ACT"
                                          'note= "encoded by TGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 39; Page 144-147; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Lee K, Belinsky M, Bain L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09361 standard; protein; 1503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                note= "encoded by
                                                                                                                          /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                  (FOXC-) FOX CHASE CANCER CENT
                                                                                                                                                                                                                                                         99WO-US006644
                                                                                                                                                                                                                                                                                                   98US-0079759P
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  'note=
                      Misc-difference 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||::|
965 GYWLSLW 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-610812/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ30081
                                                              Misc-difference
                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOAT proteins
                                                                                                                                                                    WO9949735-A1
                                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                                                                                                                                                                 27-MAR-1998;
                                                                                                                                                                                                                                                                                                                   03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            Kruh G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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AAEO9361

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The invention relates to methods and compositions for the presence of a dysfunctions. The invention is useful for screening for the presence of a dysfunctions. The invention is useful for screening for the presence of a dysfunctions. The invention is useful for screening for the presence of assectet transporter ABCC6 (MRP6-Multidrup Resistance associated protein-composition in located in the plasma membrane containing 17 membrane spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heriteable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, associated laxity and loss of elasticity, arterial insufficiency, associated with adsease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE individuals in order to identify individuals with appropriate genetic counselling in view of the PXE status. The methods are useful for connecling in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since and contain is involved in drug-resistance it is also called Multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods and compositions for diagnosing and
'note= "Nucleotide binding fold-1 (NFB-1) region"
                                                                                                                                                                                                                                                                                  'note= "Nucleotide binding fold-2 (NFB-2) region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening presence of Pseudoxanthoma elasticum mutation useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 77.8%; Score 42; DB 4; Length 1503; Local Similarity 71.4%; Pred. No. 7.7e+02; es 5; Conservative 2; Mismatches 0; Indels
                                                                      (NFB-1)
                                                                                                                                                                              1321. .1327
/note= "Nucleotide binding fold-2 (NFB-2)
1403. .1433
                                                                                                                                         (NFB-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terry S;
                                                                                                       1292. .1307
/note= "Nucleotide binding fold-2
                                                                      'note= "Nucleotide binding fold-1
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein.) CG of gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning chalces grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retinal haemorrhages leading to macular CG andiovascular disease and retinal haemorrhages leading to macular CG degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 allels who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are consumed mare area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is homen ATP-binding casette (ABCC6 (MRP6) R1314W mutant protein. Note: The present human ATP-hinding casette (ABCC) whomen ATP-hinding casette (ABCC) whomen ATP-hinding casette (ABCC) whomen ATP-hinding casette (ABCC) when human ATP-hinding casette (ABCC) when human ATP-hinding casette (ABCC) when human ATP-hinding casette (ABCC) a hinding casette (ABCC) whomen ABCCC (ABCC) when human ATP-hinding casette (ABCC) and casette caset carriers and character carriers and character carriers a
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                                                Human ATP-binding cassette transporter ABCC6 (MRP6) R1314W mutant.
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ö Gaps ö Length 1503; 0; Indels 77.8%; Score 42; DB 4; I 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Conservative Query Match Best Local Similarity GYWLTIW 7 Sequence 1503 AA;

965 GYWLSLW 971

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binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in figure 3 of the specification (AAE09361)

Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant. /note= "Wild type Val substituted with Phe" AAE09367 standard; protein; 1503 AA. Location/Qualifiers (first entry) Misc-difference 1298 mutant; mutein. WO200162977-A2. Homo sapiens. 19-NOV-2001 Synthetic. AAE09367; 

23-FEB-2001; 2001WO-US005741. 23-FEB-2000; 2000US-0184269P. 30-AUG-2001

(UYHA-) UNIV HAWAII. (PXEI-) PXE INT INC

Terry Lesaux O, Urban.Z, Boyd CD, Csiszar K,

WPI; 2001-536645/59.

N-PSDB; AAD16260

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Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.

Claim 13; Page; 163pp; English.

The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (WRP6 maps to the ATP-binding cassette transporter ABCC6 (WRP6 MILTIGING Resistance associated protein cassette transporter ABCC6 (WRP6) gene encodes a 165 kba protein located in the plasma membrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, associated Maxity and loss of elasticity individuals with one or more PXE individuals in order to identify individuals with one or more PXE counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The method are useful for the present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein. Note: The present sequence is not shown in the specification but is derived from human ATP-finner a of the present and the specification but is derived from human ATP-finner a of the present and the specification but is derived from human ATP-finner a of the present and the specification but is derived by a phone of the present and the status and the status and the status and the status and the st figure 3 of the specification (AAE09361)

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useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCCG (MRP6) G1302R mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCCG (MRP6) protein [SED ID NO: 3] shown in
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Sequence 1503 AA;

Gaps ö 77.8%; Score 42; DB 4; Length 1503; 71.4%; Pred. No. 7.7e+02; tive 2; Mismatches 0; Indels Query Match
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Search completed: January 3, 2005, 12:09:53 Job time : 153 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

January 3, 2005, 12:06:49 ; Search time 38 Seconds (without alignments) 13.962 Million cell updates/sec Run on:

1 gywltiwg 8 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

478139 segs, 66318000 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DB	ΙD	Description
-	43	79.6	492	4	US-09-107-532A-6945	Sequence 6945, Ap
7	42	77.8	1498	4	US-09-792-616-9	9
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11	37	68.5	24	4	US-09-270-767-56389	56
12	37	68.5	132	4	US-09-248-796A-22785	2278
13	37	68.5	278	4	US-09-145-828A-11	1
14	37	68.5	278	4	19-903-	18
15	37	68.5	499	4	US-09-252-991A-23328	23
16	37	68.5	591	4	-60	18
17	37	68.5	591	4	US-09-221-014-18	18,
18	37	68.5	865	4	US-09-252-991A-19339	1933
19	36.5	67.6	612	4	US-09-252-991A-19134	Sequence 19134, A
20	36	66.7	119	7	0	S
21	36	66.7	119	4	US-09-253-794-5	'n
22	36	66.7	172	4	-09-107-532A-6	9
23	36	66.7	219	ო	US-09-247-373B-52	
24	36	66.7	242	0	-80	Sequence 4, Appli
25	36	66.7	247	4		267
56	36	66.7	268	~		
27	36	66.7	280	-	US-08-414-685-2	7

15188, A	, Appli	, Appli	, Appli	, Appli	, Appli	, Appli	, Appli	Appli	, Appli	, Appli	, Appli	, Appli	, Appli				
Sequence 1:	Sequence 6	Sequence 2	Sequence 2	Sequence 4	Sequence 2	Seguence 4	Sequence 2										
US-09-248-796A-15188	US-08-463-092B-6	US-08-462-109A-6	US-08-460-907B-6	US-08-463-179A-6	US-08-461-384B-6	US-08-141-893-2	US-08-463-092B-2	US-08-463-092B-4	US-08-462-109A-2	US-08-462-109A-4	US-08-460-907B-2	US-08-460-907B-4	US-08-463-179A-2	US-08-463-179A-4	US-08-461-384B-2	US-08-461-384B-4	US-08-407-207A-2
4	-	N	~	m	٣	٦	٦	-	~	~	~	~	٣	٣	m	m	m
367	1528	1528	1528	1528	1528	1531	1531	1531	1531	1531	1531	1531	1531	1531	1531	1531	1531
66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
36		36			36			36		36	36	36	36	36	36	36	36
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS	

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Sequence 6945, Application US/09107532A
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
CRADBESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECHONE: (7191)899-5007:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...492
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 492 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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Page

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APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.9%; Score 41; DB 4; Length 222; Best Local Similarity 62.5%; Pred. No. 59; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 4;
Pred. No. 61;
2; Mismatches
                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION ONTA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 9836;
TELEFRENCE/DOCKET NUMBER: P836;
TELEPAN: (301) 309-8504
TELEPAN: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.9%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 GTWITLWG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYWLTIWG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYWLTIWG 8
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US-09-134-000C-3630
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                                                                                                                                                                                                                   Sequence 9, Application US/09792616
Sequence 9, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PIN Lecrnational, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (WRP6) causing FILE REPERENCE: PXE-001
CURRENT PAPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PIL INTERNATION:
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing TITLE OF INVENTION: Pseudoxanthoma Elasticum FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.8%; Score 42; DB 4; Length 1498; 71.4%; Pred. No. 2.8e+02; tive 2; Mismatches 0; Indels
                   DB 4; Length 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                       1; Indels
                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 408, Application US/09071035; Patent No. 6448043; GENERAL INFORMATION:
                     79.6%;
   Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1503
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
                                                                                                                              112 GYWLTCW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960 GYWLSLW 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||::|
965 GYWLSLW 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYWLTIW 7
                                                                                            1 GYWLTIW 7
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RESULT 3 US-09-792-616-3

a

LENGTH: 1498

SEO ID NO 9 TYPE: PRT US-09-792-616-9

RESULT 2 US-09-792-616-9

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RESULT 4 US-09-071-035-408

US-09-792-616-3

SEQ ID NO 3

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RESULT 8
US-09-107-532A-6868
i Sequence 6868, Application US/09107532A
i Sequence 6868, Application US/09107532A
i GENERAL INFORMATION:
i GENERAL INFORMATION:
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
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                                                                                                     Length 668;
                                                                                                                                              0; Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 4; 1
71.4%; Pred. No. 2.5e+02;
tive 1; Mismatches 1;
                                                                                                     Score 40; DB 4; Pred. No. 2.4e+02; 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...478
SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 478 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                     TYPE: PRT
CRGANISM: Candida albicans
US-09-248-796A-19350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||: |
98 GYWLSAW 104
                                                                                                                                                                                                               372 YWMTIW 377
                                                                                                                                                                                     2 YWLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-532A-6868
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Sequence 19350, Application US/09248796A

Sequence 19350, Application US/09248796A

Sequence 19350, Application US/09248796A

Sequence 19350, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER: OF SEQ ID NOS: 28208
                                                                                                       Sequence voc. Application US/09071035

Patent No. 6446043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB
Pred. No. 71;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: A Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION POR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.9%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 266 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5-
Ender Similarity 52.5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
203 GTWITLWG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 |:|:||
203 GTWITLWG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYWLTIWG 8
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                                                                                                   US-09-071-035-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 19350
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Gaps

seq32.rai

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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (6),(77),(85); OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow US-09-248-796A-22785
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APPLICANT: Mukerij, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer W.
APPLICANT: Thurmond, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REPERENCE: 6407.US.OI
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 278
TYPE: PRT
ORCANTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.5%; Score 37; DB 4; Length 278; 57.1%; Pred. No. 2.8e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.5%; Score 37; DB 4; Length 132; 100.0%; Pred. No. 1.46+02; ive 0; Mismatches 0; Indels
      DB 4; Length 24;
26;
                                                                        Indels
                                                                           3; Mismatches
         Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    Sequence 22785, Application US/09248796A Patent No. 6747137
         68.5%;
57.1%;
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Candida albicans
                                                                           4; Conservative
                                                                                                                                                                          :||::||
16 HWLSLWG 22
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Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                      2 YWLTIWG 8
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                                                                                        SECULO NO. 5673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE
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US-09-270-767-41173
Sequence 41173, Application US/09270767
Fatent NO. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41173
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-270-767-56389

Sequence 56389, Application US/09270767

Patent No. 6703491

Patent No. 6703491

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 56389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2.4e+02;
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; ORGANISM: Drosophila melanogaster
US-09-270-767-56389
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US-09-270-767-41173
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Best Local Similarity 71.4
Matches 5; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-2629
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16 HWLSLWG 22
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Matches 4; Conserv
                                       RESULT 9
US-09-540-236-2629
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Gaps

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Gaps

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Sequence 23128, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-0-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2328

LENGTH: 499
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                                                                                        RESULT 14
US-09-903-456-18

Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
APPLICANT: Abbort Laboratories
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Heenard, Amanda Eun-Yeong
APPLICANT: Heenard, Amanda Eun-Yeong
APPLICANT: Bereira, Suzette L.
ITILE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 4070.18. P.
FILE REFERENCE: 2001-07-11
PRIOR REPLICATION NUMBER: US 09/903,456
CURRENT APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SCOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.5
Best Local Similarity 57.1
Matches 4; Conservative
|||: :|
108 GYWIFLW 114
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108 GYWIFLW 114
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111 GYWISAW 117
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Job time : 39 secs

Search completed: January 3, 2005, 12:14:33

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:13:15 ; Search time 142 Seconds

(without alignments)

20.266 Million cell updates/sec
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Title:
SEG32
Perfect score: 54
Sequence: 1 gywltiwg 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1599051 segs, 359727711 residues
Total number of hits satisfying chosen parameters: 1599051
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match O*
Listing first 45 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 34, Appl	Sequence 35, Appl	Sequence 73, Appl	Sequence 297, App	Sequence 57928, A	Sequence 190740,	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 114, App	Sequence 338, App	Sequence 43458, A
	ID	US-10-046-922-34	US-10-046-922-35	US-10-125-869A-73	US-10-462-262-297	US-10-282-122A-57928	US-10-437-963-190740	US-09-792-616-9	US-10-764-328-9	US-09-792-616-3	US-10-764-328-3	US-10-125-869A-114	US-10-462-262-338	US-09-864-761-43458
	DB	13	13	14	15	15	16	10	16	10	16	14	15	0
	Query Match Length DB	10	10	13	13	474	671	1498	1498	1503	1503	14	14	34
æ	Query Match	100.0	100.0	79.6	79.6	79.6	79.6	77.8	77.8	77.8	77.8	75.9	75.9	75.9
	Score	54	54	43	43	43	43	42	42	42	42	41	41	41
	Result No.		~	٣	4	ស	9	7	8	σ	10	11	12	13

75.9	82 15 222 9 222 14 266 9	US-10-424-599-240891 US-09-071-035-408 US-10-206-576-408 US-09-071-035-406	4 4
74.1	266 14 101 15 116 10	US-10-206-576-406 US-10-424-599-194869 US-09-910-483-1	Sequence 406, App Sequence 194869, Sequence 1, Appli
	116 10	US-09-910-483-5 US-09-910-483-9	່ທ໌ດ
74.1	16 10	US-09-910-483-13	13,
74.1	10 10 10 10	US-09-910-483-11	Sequence 17, Appl
	910	US-09-910-483-25	Sequence 25, Appl
	9	US-09-910-483-33	33,
ជា	9 10	US-09-910-483-37	37,
116	101	US-09-910-483-41 US-09-910-483-43	Sequence 41, Appl Sequence 43, Appl
74.1 138	14	US-10-160-232-86	86,
138	14	US-10-160-232-90 US-10-369-493-8834	Sequence 90, Appl Sequence 8834, An
	14	US-10-125-869A-75	75, 7
72.2 13	15	US-10-462-262-299	299
	15	US-10-424-599-226815	22681
	17	88	Sequence 188067,
	14	US-10-156-761-13764	Sequence 13764, A
	σ	US-09-738-626-5178	Sequence 5178, Ap
452	14	US-10-091-007-88	Sequence 88, Appl
2 474	15	US-10-282-122A-52805	Sequence 52805, A
2 475	5 15	US-10-282-122A-57680	Sequence 57680, A
2 794	6	US-09-738-626-4579	Sequence 4579, Ap
101	1 17	US-10-425-115-260407	Sequence 260407,

## ALIGNMENTS

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WESULI' I

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Sequence 34, Application US/10046922

Sequence 34, Application US/10046922

Sequence 34, Application VISCO20164667A1

Sequence 34, Application No. US2020164667A1

GENERAL INFORMATION: EXEMINATER AND METHODS

FILE REPREMEE: 2002-01-15

TITLE OF INVENTION: VEGR-3 INHIBITOR MATERIALS AND METHODS

FILE REPREMEE: 2002-01-15

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT PELLOR DATE: 2002-01-15

SEQ ID NO 34

LENGTH: 10

SEQ ID NO 34

LENGTH: 10

TYPE: PRATURE:

NAME/KEY: SITE

LOCATION: (1) .. (1)

OTHER INFORMATION: X is any amino acid

NAME/KEY: SITE

LOCATION: (10) .. (10)

OTHER INFORMATION: X is any amino acid

UCATION: (10) .. (10)

SEQ ID NO 34

SEQ ID NO 34

SECTION: (10) .. (10)

OTHER INFORMATION: X is any amino acid

UCATION: (10) .. (10)

SECTION: (
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Oy 1 GYMLTIWG 8
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Db 2 GYWLTIWG 9

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Query Match 79.6%; Score 43; DB 15; Length 13; Best Local Similarity 62.5%; Pred. No. 10; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                       OTHER INFORMATION: immunoglobulin binding polypeptide
              FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
FRIOR APPLICATION NUMBER: US 60/388,642
FRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 57928, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Amadon, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: ApplicAnt: Obleen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Dolleen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Dolleen, Kari
APPLICANT: Dolleen, Kari
APPLICANT: Dolleen, Kari
  TITLE OF INVENTION: PROTEIN ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                            1 GYWLTIWG 8
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RESULT 2
US-10-046-922-35
Sequence 35, Application US/10046922
Sequence 35, Application US/10046922
Sequence 35, Application US/10046922
Septimental INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2867/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILIG DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE PRECEIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.22; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOSTICALE OF STATE OF SEQUENCE 73, APPLICATION US/10125869A

PUBLICATION NO. US20030199671A1

GENERAL INFORMATION:
APPLICANT: RONGON, 1508C JOSUS
APPLICANT: RANGON, C1-LONG
APPLICANT: Stochl, Mark
APPLICANT: RANGONGÉ, Thomas C.
APPLICANT: POTENEY, MIN Daniel (decessed)
ITILE OF INVENTION: BINDING MOLECULES FOR FC-REGION
ITILE OF INVENTION: BINDING MOLECULES FOR FC-REGION
ITILE OF INVENTION: BINDING MOLECULES FOR FC-REGION
ITILE OF INVENTION: BOLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/284,534
PRIOR APPLICATION NUMBER: 60/284,534
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FASESEQ for Windows Version 4.0
SOFTWARE: PRICE PRICE OF WINDOWS PERSON ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-73
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                                                                                                                                                                                                                                                                         SEQ ID NO 35
LENGTH: 10
TYPE: PRT
CORGANISM: isolated peptide
US-10-046-922-35
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Best Local Similarity 100.
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Best Local Similarity 62.5
Matches 5; Conservative
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US-10-125-869A-73
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FEATURE:

RESULT 4

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APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: Diversity of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001PC
CURRENT APPLICATION NUMBER: US/10/764,328
NUMBER OF SEQ ID AND: 27
SOFTWARE: PATENTIN PATE: 2004-01-23
NUMBER OF SEQ ID NOS: 27
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US-09-792-616-3

Sequence 3, Application US/09792616

Publication No. US20030165828A1

Publication No. US20030165828A1

PUBLICANT: PXE International, Inc.

APPLICANT: DIVERMATION: University of Hawaii

TITLE OF INVENTION: Pseudoxanthoma Blasticum

PILE REFERENCE: PXE-001

TITLE OF INVENTION: UNMERR: US/09/792,616

CURRENT APPLICATION NUMBER: US/09/792,616

CURRENT FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.0

LENGTH: 1503
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Sequence 3, Application US/10764328

Publication No. US20040166521A1

GENERAL INFORMATION:
APPLICANT: PER International, Inc.
APPLICANT: University of Hawaii
ITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
ITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PER 20016

CURRENT APPLICATION NUMBER: US/10/764,328

CURRENT FILING DATE: 2004-01-23
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Pred. No. 9.3e+02;
2; Mismatches 0
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Pred. No. 9.3e+02;
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mus musculus
US-10-764-328-9
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US-09-792-616-3
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TITUE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITUE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09792616
Publication No. US20030165828A1
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: Wiversity of Hawaii
TITLE OF INVENTION: Mucations in a gene encoding an ABC transporter (WRP6) causing;
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
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77.8%; Score 42; DB 10; Length 1498;
Best Local Similarity 71.4%; Pred. No. 9.38+02;
Matches 5; Conservative 2; Mismatches 0; Indels (
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                          Length 474;
                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_87125C.1.pep
US-10-437-963-190740
                                        79.6%; Score 43; DB 15;
85.7%; Pred. No. 2.4e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                               Sequence 19040, Application US/10437963
Publication No. US20040123343A1
GEBERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Lo, Ping
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85.7%;
                     Query Match
Best Local Similarity 85.7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
US-09-792-616-9
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94 GYWLTCW 100
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US-10-437-963-190740
US-10-282-122A-57928
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APPLICANT: Wu, Qi-Long
APPLICANT: Ecochi, Mark
APPLICANT: Stochi, Mark
APPLICANT: Stochi, Mark
APPLICANT: Stochi, Mark
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REPERBANCE: 342.1106-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT FILING DATE: 2002-11-19
FRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOCTHARR: FastSEQ for Windows Version 4.0
SEQ ID NO 114
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                                                                                                                                                                                                 2; Mismatches
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APPLICANT: Sato, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
TITLE REFERENCE: 10280-052001
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 338
                                                                                                                                                                                                                                                                                                                                                                        Sequence 114, Application US/10125869A Publication No. US20030199671A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 338, Application US/10462262; Publication No. US20040009534A1; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                          Query Match
Best Local Similarity 71.3.
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Matches 5, Conservative
                                                           ; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3
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965 GYWLSLW 971
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1 GFWCTFWG 8
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US-10-125-869A-114
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US-10-462-262-338
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US-09-664-761-41458
US-09-064-761-41458
US-09-064-761-41458
US-001-064-761-41458
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US-001-064-761-41458
US-001-061-41458
US-001-061-4145
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0
                                                                                                       Score 41; DB 15; Length 14;
Pred. No. 21;
1; Mismatches 2; Indels
; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-338
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
                                                                                                              75.9%;
62.5%;
                                                                             Query Match
Best Local Similarity 62.55,
5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                          1 GYWLTIWG 8
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Query Match 75.9%; Score 41; DB 9; I
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1;
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Job time : 143 secs
FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION DATA;
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/GENT INFORMATION:
NAME: A. Anders Brockes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98,373
REPERNEK/DOCKET NUMBER: 983692
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH. 222 amino acids
                                                                                                                                                                                                                                                                                                                                               LENGTH: 222 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-071-035-408
                                                                                                                                                                                                                                                                                                                                                                                              single
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179 GTWITLWG 186
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 240891, Application US/10424599
; Sequence 240891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Roya Thomas J
; APPLICANT: About Withus
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240891
                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 408, Application US/09071035
Publication No. US20020045737A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                   75.9%; Score 41; DB 9; Length 34; 62.5%; Pred. No. 46; 0; Indels tive 3; Mismatches 0; Indels
    ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2 CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4 US-09-864-761-43458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59551C.1.pep
US-10-424-599-240891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCIT Text

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(82)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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GYWITVFG 32
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Gaps

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Length 222;

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# GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd

- protein search, using sw model OM protein January 3, 2005, 12:03:34 ; Search time 38 Seconds (without alignments) 20.256 Million cell updates/sec Run on:

1 gywltiwg 8 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

68.5 167 2 AF0881 probable exposed to the first probable of the fi	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	SCORE 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	MACCh Lengton 77.8 15.9 15.10 75.9 15.9 15.10 75.9 15.10 75.9 15.10 72.2 4919 70.4 4416 70.4 4416 70.4 6829 70.4 1063 69.4 1063	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	000000000000000000	ID C95307 T42216 B944117 B944117 C34903 B95282 AF1978 T46745 C86879 T46745 G90251 T50103 S58888 S58888 S71847 A33830	probable transport multidrug reeistan replication protein permease [imported Ig heavy chain pre probable Nat/H+-ex probable ABC trans hypothetical prote arginine/ornitine arginine/ornitine probable integral nat/h+ antiporter ABCTransporter [im probable oxidoredu Ins P4-binding pro Ins P4-binding pro cation efflux syst cadmium, zinc, cob
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probable amino aci	arginine/ornithine	arginine/ornitine	probable transcarb	hypothetical prote	phosphatidylglycer	partial probable m	hypothetical prote	1-acyl-sn-glycerol	1-acylglycerol-3-p	hypothetical prote	GPI2 protein - yea	hypothetical prote	hypothetical prote		probable membrane
E83497	JH0110	G86878	F82966	F69990	E83140	H85756	G82391	G81013	A81957	A69843	S61111	A83779	D84541	S43540	B90862
7	~	~	7	~	~	7	~	~	~	~	7	7	~	~	0
472	482	497	607	164	171	239	241	247	247	250	280	292	351	385	387
68.5	68.5	68.5	67.6	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
37	37	37	36.5	36	36	36	36	36	36	36	36	36	36	36	36

## ALIGNMENTS

eliloti (strain 1021) mag

C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: C95307 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Status: preliminary
A;Rotestus: preliminary
A;Rotestus: preliminary
A;Rotestus: preliminary
A;Rotestus: preliminary
A;Rotestus: preliminary
A;Rotestus: 1-441 «KUR»
A;Cross-references: UNIPROT: Q922T6; GB:AE006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymA
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Coience 293, 668-672, 201.
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Titles: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Rotecter annotation

A;Genome: plasmid A;Gene: SMa0684

C;Superfamily: L-lysine transport protein

Gaps ö Length 441; 0; Indels Score 42; DB 2; Pred. No. 32; 2; Mismatches Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative ;

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|||::|| GYWISIW 98 1 GYWLTIW 7 ઠે a

multidrug resistance-associated protein homolog MLP-1 - rat

C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
A). Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DDBJ

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6; Conservative
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Matches 6; Conserv
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A;Residues: 1-419 <KUR>
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
A;Gene: SSO2718
A;Molecule type: mRNA
A;Residues: 1-1502 cHIRA
A;Cross-references: UNIPROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3
A;Experimental source: strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; AIP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E50446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                      replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Species: Pyrococcus sp.
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
R;Rashid, N.; Morikawa, M.; Imanaka, T.
R;Rashid, N.; Morikawa, M.; Imanaka, T.
A;Reference number: JC4514; MUD:96105215; PMID:8529878
A;Reference number: JC4514; MUD:96105215; PMID:8529878
A;Ression: PC4117
A;Molecule type: DNA
A;Residues: 1-391 <RAS>
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                                                                                                                                    77.8%; Score 42; DB 2; Length 1502; 71.4%; Pred. No. 1e+02; tive 2; Mismatches 0; Indels
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Pred. No. 41;
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Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
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Local Similarity 85.7%;
nes 6; Conservative
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                                                                                                                                         Query Match 77.8
Best Local Similarity 71.4
Matches 5; Conservative
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GFWETLWG 372
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964 GYWLSLW 970
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A; Status: preliminary
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probable Na+/H+-exchanging protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: B71038
B;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Reference number: A71000, MUID:98344137, PMID:9679194
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C;Species: Sinorhizoblum meliloti
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
S;Kalman, S;Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-888, 2001
A;Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizoblum meliloti
A;Reference number: A55262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA,
Mesidues: 1-508 KKUR>
A,Residues: 1-508 KKUR>
A,FResidues: 1-508 KKUR>
A,CTOSS-references: UNIPROT:0930N2; GB:AE006469; PIDN:AAK64821.1; PID:914523232; GSPDB:GR
A,Experimental source: strain 1021, megaplasmid pSymA. Abola, P.; Ampe, F.; Barloy-Hubler, R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
                                                                                                                                                                                                                                    idiotypically cross-read
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A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
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C; Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996 C; Accession: C34903
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A; Title: Active site structure and antigen binding properties of idiotypical A; Reference number: A34903, MUID:90094387; PMID:2104617
A; Accession: C34903
A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-142 < BED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;34-119/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2
Pred. No. 22;
0; Mismatches
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Best Local Similarity 62.5%;
Matches 5; Conservative
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arginine/ornitine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140 C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: C66879
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Benome Ress. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A;Reference number: A86625; WUID:21235186; PMID:11337471
A;Accession: C86879
A;Accession: C86879
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:09CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:GA;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: TJ5739
R;Saunders, D.C; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21588
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A,Residues: 1-118 <SAU>
A,Cross-references: UNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN00070; SCOED
A,Experimental source: strain A3(2)
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SCOEDB:SC7H2.08
C;Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        na+/h+ antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)
C,Species: Pyrococcus abyssi
C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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               Gaps
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               Indele
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               1;
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Pred. No. 1e+02;
1; Mismatches
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               Mismatches
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           1;
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Conservative
               5; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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GYWLSAW 100
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51 FWLSLWG 57
                                                                                   GYWLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-490 <STO>
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               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)
CiSpecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Uu1-2004
C;Accession: AF1978
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AF1978
A;Accession: AF1978
A;Accession: AF1978
A;Residues: 1-376
A;Residues:
Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandehol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUD:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:
A;Gene: SMa0302

A;Genome: plasmid
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a1r1377
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C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46745
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, A;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of A;Reference number: Z23141; MUID:98361904; PMID:9696763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2
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Pred. No. 74;
0; Mismatches 1; Indels
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A;Molecule type: DNA
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Pred. No. 79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               74.1%;
85.7%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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A; Gene: arcD C; Genetics:

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A;Reference number: A75001
A;Accession: C75176
A;Status: preliminary
A;Redeuls: preliminary
A;Residues: 1-426 < kAW>
A;Residues: 1-426 < kAW>
A;Experimental source: strain Orsay
C;Genetics: apah-2; PAB0390
C;Superfamily: Aquifex aeolicus Na+/H-exchanging protein napAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13

4867251

ABCTransporter [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: G90251
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett. R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <KUR>
A;Cross-references: UNIPROT:Q972C3; GB:AE006641; NID:g13814184; PIDN:AAK41270.1; GSPDB:C
C;Genetics:
A;Gene: SSO0999
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A;Experimental source: strain 972h(-); cosmid c1783
C;Genetics:
A;Gene: SPDB:SPAC1783.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 66.7
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Best Local Similarity
Matches 6; Conserva
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1 GYWLTIWG 8

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The P4-binding protein - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: S5888

R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irvy, Nature 376, 527-530, 1995

A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the A;Title: S58888

A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;Title: A;
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244 GRWPTIWG 251
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Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillas.
Lactobacillus.
NCBI_TaxID=33959;
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AASO8923,
02-MAR-2004 (TEMBLrel. 27,
02-MAR-2004 (TEMBLrel. 27,
02-MAR-2004 (TEMBLrel. 27,
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LJ1101.
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088269 rattus norv
095.25 homo sapien
060.694 yarrowia li
091.09 they they moplasm
097.097 sulfolobus
080mv4 synechococc
077.284 plasmodium
074.433 geobacter s
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Q8h2n7 oryza sativ
Q6mc01 parachlamyd
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Q92zt6 rhizobium m
Q8t6h2 dictyosteli
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                                                                                                             January 3, 2005, 11:52:29 ; Search time 187 Seconds (without alignments) 24.615 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
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AAS08923
Q8H2N7
Q6MC01
CAF23898
Q92ZT6
Q92ZT6
Q9T6H2
MRP6_MOUSE
MRP6_RAT
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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QGS925
QGS925
QGS920
QGRA22
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QGRA56
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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            Géc129 yarrowia 11
Q8y40 anabaena sp
Q8use pyrobaculum
Q7nsj2 chromobacue
Q9ky3 lactococcus
Q6ky1 streptococ
Aar30125 streptoco
Q6hy1 bacillus ch
Q73e85 bacillus ce
A8139409 bacillus
Q811h9 bacillus
Q53092 lactobaccill
Q8dwp9 streptococc
 Q9arz0 oryza sativ
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EMBL, AB017203; AAS08923.1; -... InterPro; IPR004254; HlyllI. related.
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                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Last annotation update)
099ARZ0
08CC129
08YX40
08ZUSB
07NSJ2
09YGV3
06TK71
AAR30325
06HP27
073EB5
0811H9
AAR39409
ARCD LACSK
                                                                                                                                                                                                                                                                                                                                       Created)
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TIGRFAMB; TIGR01065; hlyIII; 1.
                                                                                                                                                                                                                                                                                                                        Q74JK6;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                Hemolysin-like protein.
OrderedLocusNames=LJ1101;
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
2257
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GFWLLVWG 179
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=33959;
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PubMed=14966310;
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Last sequence update) Last annotation update)

Created)

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273 YWLSLWG 279
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Best Local Similarity
Matches 5; Conserv
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CAF23898;
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CAF23898
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Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
NCBI_TaxID=264201;
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                                                                                  Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Prittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; "The genome sequence of the problotic intestinal bacterium Lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL, AE017203; AAS08923.1; -- SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 43; DB 2; Length 221; 62.5%; Pred. No. 70; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 733;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005486; BAC16197.1; -
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SEQUENCE 733 AA; 82939 MW; E95884DADIDC2AC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein 001138_B05.118.
Name=001138_B05.118;
Oryza sativa (japonica cultivar-group).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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85.7%; Pred. No. 2.1e+02;
iive 0; Mismatches 1;
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Pfam; PF04578; DUF594; 1.
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hes 5; Conservative
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Les 6; Conservative
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ORFNames=pc1174;
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   FROM N.A.
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                                   STRAIN=NCC 533;
PubMed=14966310;
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OQBH2N7
OQBH2N7
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"Genome sequence of an amoeba symbiont and its use for reconstructing the evolutionary history of chlamydiae."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAF23898.1; -. Hypothetical protein.
SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of an amoeba symbiont and its use for reconstructing the evolutionary history of chlamydiae."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
NCBI_TaxID=264201;
                                                                                                                                                                                                                                                                                             Gaps
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EMBL, BX908798; CAF23898.1; -- Hypothetical protein.

SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
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Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.
Rattei T., Mewes H., Wagner M.;
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                      Score 42; DB 2; Length 284;
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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71.4%; Pred. No. 1.38+02;
.ive 2; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable transport protein.
OrderedLocusNames=RA0363; ORFNames=SMa0684;
Rhizobium meliloti (Sinorhizobium meliloti).
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Last annotation update)
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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(er) AfCS-Nature Molecule Pages (2004).
   InterPro; IPR003593; AAA ATPase.
                                                                                                                                          Pfam; PF00664; ABC membrane; 2.
Pfam; PF00005; ABC_tran; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family C, member 6).
Name=Abcc6; Synonyme=Mrp6;
                                                                                                IPR003439; ABC
                                  IPR011527; ABC_
IPR001140; ABC_
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                                                                                                                                                                                                                                                                                                                                                                          ATP-binding.
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                                                                             InterPro
                                                                                                           InterPro
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RA MEDLINE-1162136824; PubMed=11474104;
RA Galibert P., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Galibert P., Finan T.M., Long S.R., Puehler A., Botstard P., Bothe G.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Botstard P., Bothe G.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.P.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Masuy D., Palm C., Peck M.C., Poll T.M., Portetelle D., Purnelle B.,
A Masuy D., Palm C., Peck M.C., Poll T.M., Vondenbol M.,
A Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
T. "The composite genome of the legume symbiont Sinorhizobium meliloti.";
E. Science 293:668-672(201);
R. RMBL, AB007228; AAK65021:1;
R. PRI, C95307; C95307.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0000166; F:nuclectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                                         Barloy-Hubler F., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A.; Long S.R.,
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti psyma megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO:0006865; F:amino acid transport; IEA.
GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anjard C., Loomis W.F.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. - I- SIMILARITY: Belongs to the ABC transporter family. EMBL; AR47439; AAL85710.1; -. HSSP; PO8716: 1MTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 AA; 46277 MW; B6F5C9EC96011AD0 CRC64;
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Complete proteome; Plasmid; Transmembrane; Transport SEQUENCE 441 AA; 46277 MW: RAFFCOFCOANTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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Last annotation update)
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InterPro, IPR004841; Permease_region.
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                       MEDLINE=21396509; PubMed=11481432;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71...
5; Conservative
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087642
AC 08166
AC 0816
DT 01-M
DT 01
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STRAIN=FVB/N; TISSUE=Liver;

X STRAIN=FVB/N; TISSUE=Liver;

X Straubberg R.L.; Feligold B.A.; Grouse L.H.; Derge J.G.;

XBDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Straubberg R.L.; Feligold B.A.; Grouse L.H.; Derge J.G.;

X Altschul S.F.; Zeeberg B., Buerow K.H.; Schaefer C.P.; Bhat N.K.;

X Altschul S.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haich F.;

X Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haich F.;

X Brakers M.B.; Scares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

X Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

X Raha S.S.; Loquellano N.A.; Peters G.J.; Abrameon R.D.; Mullahy S.J.;

X Bosak S.A.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

X Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

X Nollalon D.K.; Muzny D.M.; Sodergren E.J.; Lu K.; Gibbs R.A.;

X Nollalon D.K.; Muzny D.M.; Sodergren E.J.; Lu K.; Gibbs R.A.;

X Nollalon D.K.; Muzny D.W.; Schevchenko Y.; Bouffard G.G.;

X Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

X Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

X Goneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBRIS7; QBOYB6;
01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
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Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
"Mus musculus mRNA for multidrug resistance-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              1308 AA; 149576 MW; 336120AC8F737AC1 CRC64;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 42; DB 2; Le
100.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1498 AA
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Beck C., Le Saux O., Varadi A., Boyd C.;
"Abcef.":
                                                                                                                                                                                         SMART; SM0382; AAĀ; 2.
PROSTIE; PSG0221; ABC_TMIF; 2.
PROSTIE; PSG0211; ABC_TRANSPORTER 1; 1.
PROSITE; PSG0893; ABC_TRANSPORTER_2; 2.
membrane 1.
TM_transpt.
transporter.
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Page

seq32.rup

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1 (By similarity).

2 (By similarity).

2 (By similarity).

3 (By similarity).

3 (By similarity).

4 (By similarity).

4 (By similarity).

5 (By similarity).

5 (By similarity).

6 (By similarity).

7 (Cytoplasmic (By similarity).

8 xtracellular (By similarity).

8 xtracellular (By similarity).

9 (By similarity).

10 (By similarity).

11 (By similarity).

12 (By similarity).

13 (By similarity).

14 (By similarity).

15 (By similarity).

16 (By similarity).

17 (By similarity).

18 xtracellular (By similarity).

19 (By similarity).

11 (By similarity).

12 (By similarity).

13 (By similarity).

14 (By similarity).

15 (By similarity). Cytoplasmic (By similarity). 16 (By similarity). Extracellular (By similarity) Extracellular (By similarity)
15 (By similarity). Cytoplasmic (By Similarity).
ABC transporter 1.
ABC transporter 2.
ATP (Potential). Cytoplasmic (By Similarity). 13 (By similarity). 17 (By similarity) ATP (Potential) InterPro; IPR003593; AAA Arpase.
InterPro; IPR00140; ABC_TM transpt.
InterPro; IPR001439; ABC_TKansporter.
InterPro; IPR005292; MRP assoc.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_tran; 2.
SWART; SM00382; AAA; 2.
IIGRPAMS; TIGR0057; MRP assoc_pro; 1. EMBL; AB028737; BAA83820.1; -. EMBL; BC049980; AAH49980.1; -. HSSP; Q03518; 1JJ7. MGD; MGI:1351634; Abcc6. 1013 1056 1077 1078 1099 1170 1191 1214 1498 851 1494 668 1057 627 1260 661 1294 079 1100 1194 DOMAIN TRANSMEM CARBOHYD CARBOHYD CONFLICT DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM FRANSMEM FRANSMEM TRANSMEM FRANSMEM FRANSMEM **TRANSMEM PRANSMEM** TRANSMEM TRANSMEM **TRANSMEM** TRANSMEM FRANSMEM **TRANSMEM** DOMAIN NP BIND BIND DOMAIN DOMAIN DOMAIN NIWWO DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN OMAIN DOMAIN OMAIN DOMAIN DOMAIN DOMAIN 

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6) (MRP-like protein-1) (MLP-1).
Name-Abcc6; Synonyms-Mrp6, Mlp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Pharmacol. 57:634-641(2000).
--- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly (By similarity).
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- TISSUE SPECIFICITY: High in liver and lower in duodenum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Hepatic expression of multidrug resistance-associated protein-like proteins maintained in eisai hyperbilirubinemic rats."; Mol. Pharmacol. 53:1068-1075(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-20159081; PubMed-10692506;
Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger B.;
"Transport function and hepatocellular localization of mrp6 in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-98279126; PubMed-9614210;
Hirohashi T., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
                                                                                                                                           ö
                                                                                                        DB 1; Length 1498;
                                                                                                        Score 42; DB 1; Length 149
Pred. No. 5.9e+02;
2; Mismatches 0; Indels
I -> T (in Ref. 2).

H -> Q (in Ref. 2).

L -> V (in Ref. 2).

N -> S (in Ref. 2).

MW; BPCPF33F0EEC813C CRC64;
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InterPro; IPR001140; ABC_IM_transpt.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR05292; WRP_assoc.
Pfam; PF000664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
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 927 927 I
1401 1401 H
1448 1448 I
1477 1477 h
1498 AA; 164788 MV
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                                                                                                        77.8%;
                                                                                                                          71.4%;
                                                                                                                                             5; Conservative
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Best Local Similarity
Matches 5; Conserv
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088269;
   CONFLICT
                                     CONFLICT
                                                                        SEQUENCE
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305255; P78420; Q9UMZ7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 45, Last annotation update)
Multidarug resistance-associated protein 6 (Affe-binding cassette, family C, member 6) (Anthracycline resistance-associated (Multi-specific organic anion tranporter-E) (MOAT-E).
Homo sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlcNAc. . .) (Potential)
MW; 539901B674A74A28 CRC64;
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                                          PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS50893; ABC TRANSPORTER 2; 2.
ATP-binding; Glycoprofein; Repeat; Transmembrane; Transport.
                                                                                                                                        Cycoplasmic (By similarity).
2 (By similarity).
2 (By similarity).
3 (By similarity).
Cytoplasmic (By similarity).
Cytoplasmic (By similarity).
4 (By similarity).
Extracellular (By similarity).
5 (By similarity).
Cytoplasmic (By similarity).
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                                                                                                            Extracellular (By similarity)
                                                                                                                                                                                                                                                                                     6 (By similarity).
Extracellular (By similarity)
7 (By similarity).
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Extracellular (By similarity)
9 (By similarity).
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Extracellular (By similarity)
11 (By similarity).
Cytoplasmic (By similarity).
12 (By similarity).
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Extracellular (By similarity)
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Cytoplasmic (By similarity).
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Cytoplasmic (By similarity).
ABC transporter 1.
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ABC transporter 2.
ATP (Potential).
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N-linked (GlcNAc.
ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 2.
IIGRFAMB; TIGR00957; MRP_assoc_pro; 1.
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Best Local Similarity 71...
For 5, Conservative
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1502 AA;
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GYWLSLW 970
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MRP6 HUMAN
MRP6 HUMAN
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DT 30-MA
DT 30-MA
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DE Multi
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GN Name
CC BUKAR
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MEDLINE=21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200; Ilias A., Urban Z., Seidl T.L., Le Saux O., Sinko E., Boyd C.D., Sarkadi B., Varadi A.; Iloss of ATP-dependent transport activity in pseudoxanthoma elasticumassociated mutanis of human ABCC6 (MRP6).";
                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.

MEDLINE=99425270; PubMed=10493829;

MEDLINE=99425270; PubMed=10493829;

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,

Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

Bichler B.E., Harris P.C., Venter J.C., Adams M.D.;

"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";

Genomics 60:295-308(1999).
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DOI=10.1002/1098-1004(200011)16:5<449::AID-HUMU24>3.0.CO;2-O;
Germain D.P., Perdu J., Remones V., Manzoni K., Jeunemaitre X.;
"Identification of two polymorphisms (c189G>C; c190T>C) in exon 2 of
the human MRP6 gene (ABCC6) by screening of Pseudoxanthoma elasticum
patients: possible sequence correction?";
Hum. Mutat. 16:449-449(2000).
[1] SEQUENCE FROM N.A.
MEDLINE=9910722; PubMed=9892204;
Kool M., van der Linden M., de Haas M., Baas F., Borst P.;
Kool M. ton der Linden M., de Haas M., Baas F., Borst P.;
Expression of human MRP6, a homologue of the multidrug resistance protein gene MRP1, in tissues and cancer cells.";
Cancer Res. 59:175-182(1999).
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Belinsky M.G., Kruh G.D.;
"MOATE E (ARA) is a full-length MRP/cMOAT subfamily transporter expressed in kidney and liver.";
Br. J. Cancer 80:1342-1349(1999).
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SEQUENCE FROM N.A.
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Tipopoteins."; Abore gene potywintpubmic absociated with variation in plasma in inporteins."; Abore gene potywintpubmic discrete with Genet. 46:699-705(2001).

1. FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly. Transports glutathione conjugates as Leukotriene-C4 (LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).

2. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

2. Integral SPECIFICITY: Expressed in kidney and liver. Very low expression in other tissues.

3. Integral SPECIFICITY: Expressed in kidney and liver. Very low expression in other tissues.

4. Integral SPECIFICITY: Expressed in kidney and liver. Very low expression in other tissues.

5. Integrals: Defects in ABCC6 are a cause of autosomal dominant pseudoxanthoma elasticity, arterial insufficiency and retinal hemorrhages leading to macular despensation.

6. Integrals: Defects in ABCC6 are a cause of autosomal recessive pseudoxanthoma elasticum (AR-PSE) [MIM:264800].

7. SERASE: Defects in ABCC6 are a cause of autosomal recessive pseudoxanthoma elasticum (AR-PSE) [MIM:264800].

8. SERASE: SERASE: Defects in ABCC6 are a cause of autosomal recessive consous and nose in a manual and a model prediction.

8. SERASE: SERAS
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TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHB-1298; ILE-1301; ARG-1302;
PRO-1303; GLN-1314; PRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-1361
AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319;
LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268.
MEDLINE-21426347; PubMed=11536079;
Le Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C.,
Goering H.H.H., Johnson E.W., De Paepe A., Pope F.M.,
Pasquali-Ronchetti I., Bercovitch L., Terry S., Boyd C.D.;
A spectrum of ABCC6 mutations is responsible for pseudoxanthoma
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NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/abcc6mut.htm"
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                                                                                                                                                                                                                                                 MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297; Ringpfeil F., Lebwohl M.C., Christiano. A.M., Ulitto J.; Ringpfeil F., Lebwohl M.C., Christiano. A.M., Ulitto J.; Pseudoxanthoma elacticum: mutations in the MRP6 gene encoding a transmembrane ATP-binding cassette (ABC) transporter.";
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Wang J., Near S., Young K., Connelly P.W., Hegele R.A.;
"ABCC6 gene polymorphism associated with variation in plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000)
                                                                                                                                                                                   JARIANT PXE TRP-1138, AND VARIANT GLN-1268.
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EMBL; U91318; AAC15785.1; ALT_SEQ.
EMBL; AF168791; AAD51293.1; -.
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elasticum.";
Nat. Genet. 25:223-227(2000)
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HSSP; P08716; 1MT0. Genew; HGNC:57; ABCC6. MIM; 603234; -.

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R GO; GO:0005624; C:membrane fraction; TAS.
R GO; GO:0005624; C:membrane; TAS.
R GO; GO:0005624; E:MPP binding; TAS.
R GO; GO:0005214; F:MPP binding; TAS.
R GO; GO:0005215; F:MPP-binding; TAS.
R GO; GO:0005215; F:Tesponse to drug; TAS.
R GO; GO:0006310; P:transporter activity; TAS.
R InterPro; IPR003149; ABC_TMATPAS.
R InterPro; IPR003140; ABC_TM transpt.
R InterPro; IPR005224; MRP assoc.
R Ffam; PF00664; ABC_membrane; 2.
R Ffam; PF000605; ABC_tran; 2.
R FAMRT; SM00382; AAA; 2.
R FYCDOM; PD000006; ABC_TMA; 2.
R FYCDOM; PS00039; ABC_TMANSPORTER_1; 2.
R ROSITE; PS50929; ABC_TRANSPORTER_1; 2.
R ROSITE; PS50893; ABC_TRANSPORTER_2; 2.
R ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;
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MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banarjel L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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Extracellular (By similarity).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                          OrderedLocusNames=Ta0692;
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                                                                                                                       Thermoplasma acidophilum.
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                                                                                                                                                                                             NCBI_TaxID=2303;
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangell L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekata F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Cauddron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last anno
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Praser C.M.;
"Rolle of mobile DNA in the evolution of vancomycin-resistant
Enterococcus faecalis ";
Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                75.9%; Score 41; DB 2; Length 266; 62.5%; Pred. No. 1.7e+02; ive 2; Mismatches 1; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382129; CAG82338.1; -.
SEQUENCE 376 AA; 41206 MW; E085FF7C32379DCB CRC64;
                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 266 AA; 28291 MW; CD6E72C4DF555A36 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                              EMBL; AE016957; AA082859.1; -. TIGR; EF3185; -.
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Best Local Similarity 62.5
Matches 5; Conservative
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RESULT 12
06 CBB4
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10 01-0C
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13 01-0C
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Matches

ઠ 셤 RESULT 13 O9HKA9 ID QS AC QS DT 01

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She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewep A., Graml W., Santos-Mawee H.-W., Brishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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                                                                                               Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
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Last annotation update)
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62.5%; Pred. No. 2.5e+02;
tive 2; Mismatches 1;
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EMBL, AL445065; CAC11830.1; -.

GO; GO:0015021; C:integral to membrane; IEA.

GO; GO:0015215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR007114; MFS.
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GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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InterPro; IPR005828; Sub_transporter.
Pfam; PF00083; Sugar_tr; 1.
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STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed=11427726;
Transport protein related protein.
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STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
NARAmura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Antanaba A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Antanaba A., Iriguchi M., Matsunob M., Matsuno A., Nakazaki N., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
XI Tomplete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res 9:123-130(2002).
SIRBL; AP005369; BAC07560:1; -.
DR FIRL; AP00535; Glycos_transf_2; 1.
R InterPro; IPRO173; Glycos_transf_2; 1.
KW Complete proteome.
SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;
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75.9%; Score 41; DB 2; Length 419; 62.5%; Pred. No. 2.6e+02; tive 2; Mismatches 1; Indels
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QBDMV4;
QBDMV4;
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QBDMV4;
QBDMV2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cellulose synthase.
Cellulose synthase.
CofferediocusNames=Ll10007;
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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Best Local Similarity 85.7
Matches 6; Conservative
                                           Best Local Similarity 62.5
Matches 5, Conservative
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365 GFWETLWG 372
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Search completed: January 3, 2005, 12:13:06 Job time : 190 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein January 3, 2005, 12:13:55 ; Search time 148 Seconds (without alignments) 19.391 Million cell updates/sec Run on:

SE032

Title: Perfect score:

1 gywltiwg 8 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

153769 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_23Sep04:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	lon	VEGFR-3 b	VEGFR-3 b	Somatosta	Backbone	Antigenic	Endotheli	Endotheli	Antigenic	Tyrosine	HIV A11 m	HIV A03 s	HIV B62 B	HIV A03 m	HIV A03 m	HIV A02 8	HIV A03 8	HIV B27 8	HIV All m	DENSIN-18	Cyclic an	Cyclic an	Cyclic an	Anti-micr	Anti-micr	Anti-micr
-	Description	Abp53964	Abp53965	Aay76794	Abp53418	Aaw97529	Aar29452	Aar69224	Aaw56531	Ad j 25834	Abp22594	Abp14287	Abp18686	Abp20292	Abp19992	Abp12050	Abp14288	Abp16999	Abp22402	Ad117320	Adh62133	Adh62029	Adh62062	Adp67844	Adp67877	Adp67948
		ABP53964	ABP53965	AAY76794	ABP53418	AAW97529	AAR29452	AAR69224	AAW56531	ADJ25834	ABP22594	ABP14287	ABP18686	ABP20292	ABP19992	ABP12050	ABP14288	ABP16999	ABP22402	ADL17320	ADH62133	ADH62029	ADH62062	ADP67844	ADP67877	ADP67948
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ADQ28160 ADQ28097 AAC28097 AAC28067 AAC3138 AAC31142 ADE62034 ADH62033 ADH62043 ADH62043 ADH62065 ADH62065 ADH67858 ADP67880 ADP67851 ADP67851 ADP67851 ADP67851 ADP67851 ADP67851 ADP67851	ADQ28099 ADQ28073
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 45

## ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:67. Ŕ ABP53964 standard; peptide; 7 (first entry) 09-JAN-2003 ABP53964; ABP53964

XXX
ABP5
XX RESULT 1

sapiens. Synthetic. Ношо

Key Location/Qualifiers Misc-difference 4. .6 /note= "X is any amino acid"

WO200257299-A2.

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

17-JAN-2001; 2001US-0262476P.

(LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.

Kubo H; Koivunen E, Alitalo K,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 21; Page 81; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VBGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,

antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the

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Gaps

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Score 33; DB 5; Length 8; Pred. No. 1.7e+06; Mismatches 3; Indels

61.1**%**; 57.1**%**;

present invention

Sequence 8 AA;

4; Conservative

1 GYWLTIW 7

1 GYWXXXW

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Query Match
Best Local Similarity
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antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and disease of neovascularisation, e.g. liver diseases, hypertension, post-trauma, orbitalis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis, lymphangiogenesis, vascular endothelial growth factor, cytostatic, hepatotropic, antiinflammatory, hypotensive; antidiabetic; vulnerary; cell surface receptor; cencer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated peptide (I) that binds to inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor receptor 3 inhibitor; VEGFR-3;
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                                                                                                                                                                                                            Score 33; DB 5; Length 7; Pred. No. 1.7e+06; 0; Mismatches 3; Indels
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'note= "X is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGFR-3 binding peptide SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 81; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                              ABP53965 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001US-0262476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2002; 2002WO-IB000099
                                                                                                                                                                                                              61.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                          Similarity 57... 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST (
(LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-691521/74.
                                                                                                                                                                                                                                                                       GYWLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 4
                                                                                                                                                                                                                                                                                                    GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200257299-A2
                                                                                                                                                                                Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           ABP53965;
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                           Matches
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Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclarosis; restenosis; post-aurgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretion
the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has one building unit containing a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclized somatostatin analogs for inhibiting growth hormone from anterior pituitary and as antiproliferative agents for of tumors.
                                                                                                                                                                                                                                                                                                            'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gellerman G;
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                   Somatostatin analogue peptide 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 61; 82pp; English.
                           AAY76794 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                           /note= "Trp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-IL000329.
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98US-00203389
                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hornik V, Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-136888/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEPT-) PEPTOR LTD.
                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1999;
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                                                                                      20-APR-2000
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                                                                                                                                                                                                                                                    Synthetic
                                                        AAY76794;
RESULT 3
               AAY76794
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group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders cuch as cancers, autoimmune diseases, endocrine disorders, disbeticases parcreatitis, atherosclerosis, restenosis and post-surgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogues can be used for diagnosing cancer. The backbone cyclic analogues can be used for the treatment patients with hormone-secreting analogues can be used for the treatment patients with hormone-secreting analogues can be used for the treatment patients with mormone-secreting analogues can be used for the treatment patients with dormone-dependent tumours. They reduce diarrhoes through the inhibition of vaccactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent clabates mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatospin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; charerstarberosels; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis; pancreatitis; post-surgical pain.
disulphide. At least one building unit is connected via a bridging
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 3; Length 7; Pred. No. 1.7e+06; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-terminally modified with Fmoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorenylmethoxycarbonyl)"
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP53418 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                             59.3%;
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99WO-IL000329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HORN/) HORNIK V.
(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
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15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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(GELL/)
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Gellerman G;

Hornik V, Afargan MM,

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The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

amoiety elected from the group consisting of a second building unit,

the side chain of an amino acid residue of the second building unit,

the side chain of an amino acid residue of the second building unit,

amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,

cytostatic, antidiabetic, antiinflammatory and analgesic activities, and

can be used as a somatostatin receptor ligand. (I) are useful in the

treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine disorders, inflammation,

gastrointestinal disorders, pancreatities, post-surgical pain, and

restenosis. (I) can also be used in the diagnosis of cancer, by imaging

the existence of metastases, it being labeled with a detectable probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a backbone cyclised somatostatin analogue from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            one virus epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW97452-571 represent antigenic sites derived from the haemagglutinin-
neuraminidase (HN) protein of the paramyxoviridae. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic site, haemagglutinin-neuraminidase, HN; paramyxoviridae, virus epitope, attachment protein, vaccine, immunodominant epitope.
                                               New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 5; Length 7; Pred. No. 1.7e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated proteinaceous substance - comprising at least derived from an attachment protein of a paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigenic site of HN protein loop beta-4L23.
                                                                                                   Example 12; Page 21; 30pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97529 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-00202100.
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              WPI; 2002-681319/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYWLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYWKVCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1998;
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Matches
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(WARN ) WARNER LAMBERT CO.
 4; Conservative
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Best Local Similarity
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                           3 WLTIW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLTIW 7
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                                                       1 WLDIW
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                                                                                                                                                                                                                                                                                                                                                                                      WO9414843-A1
                                                                                                                                                                                         25-MAR-2003
06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-1994
                                                                                                                                                                                                                                                                   Endothelin;
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                               AAR69224;
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                                                                                                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                             Hypertension; myocardial infarction; congestive heart failure; endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias; acute renal failure; preeclampsia; diabetes; metabolic; endocrinological; neurological; disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) used as endothelin antagonists - for treating hypertension, metabolic and endocrine disorders, heart failure, diabetes, asthma, neurological disorders, etc.
describes 3-D models identifying a proteinaceous substance comprising at least one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. The antigenic sites can be used to produce vaccines, to detect the viruses, and to select the immunodominant epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The peptide is an endothelin antagonist useful in controlling hypertension, myocardial infarction, congestive heart failure, endot shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal failure, preeclampsia, diabetes and metabolic, endocrinological and neurological disorders. Administration is oral parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be prepared by conventional peptide synthesis. (Updated on 25-MAR-2003
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                                                                                                                                                0; Indels
                                                                                                                   57.4%; Score 31; DB 2; Length 8; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5;
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Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                    AAR29452 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Ac-D-Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 95; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cody W1, Depue P, Doherty AM,
                                                                                                                                                                                                                                                                                                                                                                                      Endothelin antagonist peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-US003408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00809746
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80.0%;
                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                     Query Match
Best Local Similarity luv...
5, Conservative
                                                                                                                                                                                                                                                                                                                                             (revised)
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Best Local Similarity
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YWLTI 8
                                                                                                                                                                               YWLTI 6
                                                                                         Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9220706-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1991;
                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
13-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                AAR29452;
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ID AAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hexa:peptide derivs. inhibiting endothelin - for treatment of e.g. renal failure, hypertension, asthma, restenosis, angina, cancer etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                 Endothelin C-terminal peptide analog, useful as antagonist.
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Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Не ЛХ,
                                                                                                                                                                                                                                                                                                           ET-1; receptor; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Ac-D-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 119; 146pp; English
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AAR69224 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doherty AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-US012377.
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ilarity 80.0%;
Conservative
                                                                                                                              (revised)
(first entry)
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ID AAW!
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AAW56531;

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HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vbu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying a ligand that can mediate the biological activity of target protein via inhibition of the binding of target protein to a binding partner ligand comprising screening first combinatorial library having first member ligands for binding to target protein to identify target-binding ligands for mediate the biological activity of target protein to identify target-binding ligands the can mediate the biological activity of target proteins via inhibition of the binding of target protein to a binding partner ligand. The invention does not require that the natural binding partner be used as reagent. The need for the natural binding partner we with the use of complementary combinatorial libraries. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                          Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
                                                                                                                                                                                                                 Hyde-Deruyscher RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 8; I
Pred. No. 1.7e+06;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                           Example 5; SEQ ID NO 94; 98pp; English
                                                                                                                                                                                                                   Frelinger JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP22594 standard; peptide; 8 AA.
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                                                                                                            97WO-US019638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.7%;
                                                       98US-00069827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000; 2000WO-US027766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00412863
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(first entry)
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                                                                                                                                                                                                                 Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                                                                          (KARO-) KARO BIO AB.
                                                                                                                                                                                                                                                        WPI; 2004-068186/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YWWPDWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
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                                                         30-APR-1998;
                                                                                                                31-OCT-1997;
31-MAR-1998;
                                                                                            31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2003
15-JUL-2002
                    09-SEP-2003
                                                                                                                                                                                                                 Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001
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Best Local S
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XBXBXBXBXSXBXBXBXBXXBXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW56525-36 represent antigenic Human immunodeficiency virus type 1 (HIV-
1) peptides used in the test device of the invention. This test device
comprises, in a housing, an absorbent pad, a reagent layer containing
immobilised test antigens and a filter. The housing has an opening,
adjacent to the filter, for applying an aqueous sample, and the filter is
held in contact with the reagent layer by a sleeve. The filter protrudes
from the sleeve such that it exerts a greater pressure on the reagent
layer than does the sleeve. The device is specifically used to detect HIV
infection from presence of specific antibodies in whole blood, but many
other analytes can also be detected, e.g. amino acids, nucleic acid,
hormones, vitamins, microbial pathogens and drugs (therapeutic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unagnostic test device - provides homogeneous fluid flow and increased chemical resistance, especially for detecting antibodies to human immunodeficiency virus.
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                                                                           Antigenic HIV-1 peptide used in diagnostic test device of invention.
                                                                                                              HIV-1; antigen; test device; detection; HIV infection; antibody;
whole blood; hormone; vitamin; microbial pathogen; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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complementary combinatorial library; tyrosine tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 2; Length 5;
Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine tRNA synthetase binding peptide group 2 motif
                                                                                                                                                                                                                                                                                                                                                                                                             (UVHE-) UNIVERSAL HEALTHWATCH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 39; Page 36; 50pp; English.
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                                                                                                                                                                                              Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                    96US-0026681P.
97US-00912580.
                                                                                                                                                                                                                                                                                                             97WO-US017129
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80.0%;
                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernstein D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-230723/20.
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Best Local Similarity
Matches 4; Conserv
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LTVWG 5
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18-AUG-1997;
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                                    06-AUG-1998
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                                                                                                                                                                          Synthetic.
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ADJ2583

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Gaps

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Length 7; 3; Indels

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ABR25397). (1) has virucide activity and carb sequences (ABR25397). (1) has virucide activity and carb be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, can group-based vaccine may be selected from conserved regions of viral or uncur-associated antigens, which therefore reduces the likelihood of the antigens. Furthermore, immunosuppressive groups frat may be present on whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                           The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to
                                                                                      Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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 Chesnut R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 4; Length 8; Pred. No. 1.7e+06; 1; Mismatches 0; Indels
Southwood S, Livingston BD,
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Southwood S, Livingston BD,
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV A03 super motif env peptide #27.
                                                                                                                                            Claim 32; Page 332; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP14287 standard; peptide; 8 AA.
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80.0%;
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(first entry)
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 Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidney J,
Celis E,
                                                   WPI; 2001-354887/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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15-JUL-2002
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Baker DM,
   Sette A,
Baker DM,
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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL2347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or unmour-associated antigens, which therefore reduces the likelihood of two-based vaccine may be selected from conserved regions of viral or unmour-associated antigens, which therefore reduces the likelihood of composition and advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 4; Length 8;
Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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Kubo RT, Grey HM;
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                                                                                                        Claim 32; Page 161; 448pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.7%;
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Celis E,
                WPI; 2001-354887/37
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Best Local Similarity
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Baker DM,
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                                                                                     The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL2347 to ABR25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole cantigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in argoup-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutantes. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Applison of the present repetice used in the examplification of the present in the examplification of the present in the examplatication of the present in the examplatication of the present in the examplation of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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              compositions comprising human immunodeficiency virus-1 (HIV-1) groups, useful for vaccinating against HIV-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 4; Length 8;
Pred. No. 1.7e+06;
L; Mismatches 0; Indels
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Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                             Claim 32; Page 252; 448pp; English
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Celis E,
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15-JUL-2002
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Baker DM,
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Matches
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ABP20292
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Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined anno acid sequences (ABD25397).

CABD25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of compositional vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune seased uscaine may be selected from conserved regions of viral cumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosupressive groups fart may be present of n whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, chieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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Pred. No. 1.7e+06;
peptide groups, useful for vaccinating against HIV-1.
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Kubo RT, Grey HM;
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                                               Claim 32; Page 285; 448pp; English
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80.0%;
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15-JUL-2002 (first en
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Celis E,
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Baker DM,
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ABP19992
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                                                     The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL55347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine antigens is directed largely toward variable response to whole antigens is directed largely toward variable response to whole allowing for immune escape due to mutations. The articularion an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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Kubo RT, Grey HM;
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Claim 32; Page 279; 448pp; English
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Best Local Similarity 80.vv,
A; Conservative
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Celis E,
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LTVWG 6
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15-JUL-2002
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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequences selected from 51 defined amino acid sequences (ABL25347 to ABP2539). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, can group-based vaccine may be selected from conserved regions of viral or an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of tescape mittants Purthermore, immunosuppressive groups that may be present of additional advantage of an group-based vaccine approach is the ability to combine selected groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar enhanced cimmunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar enhanced cimmunogenicity peptide sequences used in the examplification of the present represent peptide sequences used in the examplification of the present represent peptide on 11-SEP-2003 to standardise OS field)
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Best Local Similarity
Matches 4; Conserv
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Search completed: January 3, 2005, 12:27:56 Job time : 150 secs

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Sequence 12, Appl
Sequence 1495, Ap
Sequence 1495, Ap
Sequence 1650, Ap
Sequence 27, Appl
Sequence 3, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 1500, Ap
Sequence 6, Appli
Sequence 1500, Ap
Sequence 1500, Ap
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Sequence 1649, Ap
Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
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9, Appli
1655, Ap
5, Appli
21, Appl
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                                                                                                                               January 3, 2005, 12:23:00 ; Search time 37 Seconds (without alignments) 14.339 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-315-304B-1649
US-09-319-571-12
US-08-586-670A-17
US-09-082-279B-1495
US-09-350-641C-1650
US-08-415-099A-3
US-08-415-099A-3
US-08-415-099A-3
US-08-415-099A-3
US-08-45-099A-3
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US-08-660-747-56
US-09-125-641-1
US-09-125-641-2
US-08-481-968A-19
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Maximum Match 100%
Listing first 45 summaries
                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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                    Copyright
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Maximum@DB_seq@length; 8.1.7
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Perfect score:
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US-08-154-712B-19 US-09-947-925A-19 US-09-947-925A-19 US-08-753-750B-38 5185431-15 US-07-118-577-6 US-09-082-279B-653 US-09-315-304B-653 US-09-315-304B-1579 US-09-315-304B-1579 US-09-315-305-653 US-09-515-965A-653 US-09-515-965A-653 US-09-515-965A-653 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53 US-09-563-22C-53	ALIGNMENTS	bin P TION OF DRUGS USIN ARY COMBINATORIAL MARK, P.L.L.C. N.W., Suite 300  MS-DOS #1.0, Version #1 /069,827A /050,359 S97/19638 /740,671 05 FOWLKES=4C
80 80 80 80 80 80 80 80 80 80 80 80 80 8		TIT 1  GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: FRELINGER, Jeffrey HYDE-DERUYSCHER, RO TITLE OF INVENTION: IDENTIFICA COMPLEMENT NUMBER OF SEQUENCES: 178 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEI STREET: 624 NINTH Street COMPUTRY: U.S.A. ZIP: 20001 ZIP: 20001 ZIP: 20001 ZIP: 20001 COMPUTRY: IB PC COMPATION WEDIUM TYPE: Floppy disk COMPUTRY: IB PC COMPATION COMPUTRY: IB PC COMPATION APPLICATION DATA: APPLICATION NUMBER: US/09 FILING DATE: 30-Apr.1998 APPLICATION NUMBER: US 09 FILING DATE: 31-COT-1996 ATTORNEY/AGENT INFORMATION: TELEPAX: (202) 737-3528 INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHASACTERISTICS: LENGTH: 7 amino acids TYPE: Application NOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO
प्याप्य प्राप्य प्राप्य प्राप्य प्राप्य प्राप्य D D प्राप्य प्राप्य प्राप्य प्राप्य प्राप्य य प्राप्य प्राप्य प्राप्य प्राप्य प्राप्य प्राप्य		Application (617114 FIGORMATION: CANT: FOWLKES CANT: FRELING FRELING FRELING HYDE-DE SPONDENCE ADD ADDRESSEE: BR SCONDENCE ADD ADDRESSEE: BR STREET: 624 N CITY: Washing STREET: 0.0. STREET: 0.0. STREET: DR COUNTRY: U.S. ZIP: 20001 TELE DOOR APPLICATION N FILING DATE: CLASSIFICATION N FILING DATE: APPLICATION N FILENGTH: 7 amino a STREEFAM: (202 N TYPE: amino a STREEFAM: (202 N TYPE: amino a STREEFAM: (202 N TYPE: AMINO BUSS: TYPE: AMINO BUSS: TYPE: DESCRIPTI
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NAME: Boudreaux, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M01718
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                     TOPOLOGY: circular;
MOLECULE TYPE: peptide
US-08-191-571-12
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TOPOLOGY: circular
MOLECULE TYPE: peptide
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TELEX: 2:
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Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Merutka, G.

APPLICANT: Amerika, G.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

TITLE OF INVENTION: PROPERTIES

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT PILING DATE: 1999-05-20

CURRENT PILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-05-20

WUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastEED for Windows Version 3.0
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                                       53.7%; Score 29; DB 4; Length 7; 57.1%; Pred. No. 3.8e+05; Live 0; Mismatches 3; Indels
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Patent No. 5521156

GENERAL INFORMATION:

APPLICANT: Kudlacz, Elizabeth M

APPLICANT: Buck, Stephen H

APPLICANT: Arbeson, Scott L

TITLE OF INVENTION: Cyclic Neurokinin A Antagonists

VOMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marion Merrell Dow Inc.

STATE: Ohio

STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPRY: United States
ZIP: 45215-6300
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,571
FILING DATE: 03-FEB.1994
CLASSIFICATION: 514
                   Query Match
Best Local Similarity 57.13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%,
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1 WNSLWG 6
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US-09-315-304B-1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: HIV-1
US-09-315-304B-1649
     US-09-069-827A-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pCT-US95-00296-12
; Sequence 12, Application PC/TUS9500296
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marion Merrell Dow Inc.
STREET: 2110 East Galbraith Road, P.O. Box 156300
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M01718A WO
TELEPHONE: 513-948-6566
TELEPAX: 513-948-7961 or 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BOUDTERUX, William R
REGISTRATION NUMBER: 35,796
REFERENCE/OOCKET NUMBER: M01718;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-6566
TELEFAX: 513-948-6761 or 4681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 71.4%;
Matches 5; Conservative
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50.0%;
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: HIV-1
US-09-082-279B-1495
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US-09-834-784-1495
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US-09-350-641C-1650
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LOCATION: 1..2
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "Phe is in the D conformation and is
OTHER INFORMATION: linked to DTPA;
FRATURE:
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
OTHER INFORMATION: D conformation; Tabel
FEATURE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Variant residues
/note= "The Phe is in the D conformation; Xaa
is L-4-chlorophenylalanine; the Trp is in the
D conformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Variant residues
/note= "The carboxyl group of the C-terminal
Thr is reduced to an alcohol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-UOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,670A
FILING DATE: 22-APR-1996
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6241965nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-DD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ocide
TELEX: 910-221-3317
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TOPOLOGY: linear
MOLOGY: linear
               Sequence 17, Application US/08586670A
Patent No. 6241965
GENERAL INFORMATION:
APPLICANT: MCBEIGE, William
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Somatcatin Derivatives
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
CITY: LL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-082-279B-1495
Sequence 1495, Application US/09082279B
; Patent No. 6258782
                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 80.0-
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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US-08-586-670A-17
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Batent No. 6656906

GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
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APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Aneutka, Gene
APPLICANT: Anewer, Mohmed
TITLE OF INVENTION: HYBEID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: 1972-043
CURRENT PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOPTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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US-09-834-784-1495

Sequence 1495, Application US/09834784

Patent No. 6562787

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Anwer, Mohmed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 787-043

FILE REPERENCE: 787-043

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR PLING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FBSESEQ for Windows Version 3.0

SROTUM. PRIOR PLING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 3; 1
Pred. No. 3.8e+05;
2; Mismatches 1
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Sequence 4, Application US/08415099A

Patent No. 5789384

GENERAL INFORMATION:

APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.

APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.

TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cytoven
STREET: 110230 N.E. Points Drive, Suite 530

CITY: Kirkland
STATE: Washington
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                               COUNTRY: USAN

ZIP: 98033
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage
COMPUTER: IBM PC/486 Compatible
OPERATING SYSTEM: MS-DOS 5.01
SOFTWARE: Word for Windows 6.0-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,099A
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-UU1-1994
APPLICATION NUMBER: US 08/26,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-889-5804 (direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY.

ZIP: 98033

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage compuTER: IBM PC/486 Compactible

OPERATURE SYSTEM: MS-DOS 5.01

SOFTWARE: Word for Windows 6.0-t

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/415,099A

FILING DATE: 31 MAR-1995

TASSTPICATION: 514
                                  ADDRESSEE: Cytoven
STREET: 10230 N.E. Points Drive, Suite 530
CITY: Kirkland
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 48.1%;
Similarity 60.0%;
3; Conservative
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; IMMEDIATE SOURCE:
US-08-415-099A-3
  NUMBER OF SEQUENCES: 4
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Best Local Similarity
Matches 3; Conserv
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; Sequence 3, Application US/08415099A
; Sequence 3. Application US/08415099A
; Patent No. 5789384
; Patent INFORMATION:
; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov,V.G.
; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-DEC-1993
FILING DATE: 03-UNU-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 1; Length 5;
Pred. No. 3.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 27; DB 4; Length 8; 50.0%; Pred. No. 3.8e+05;
FILE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR PRILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 27, Application US/08353400; Patent No. 566357
GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                             Query Match 50.0
Best Local Similarity 50.0
Matches 3; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::||
WDSLWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 WLTIWG 8
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                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: HIV-1
                                                                                                                                                                                                                                                                                                                        US-09-350-641C-1650
                                                                                                                                                                                                                              SEQ ID NO 1650
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US-08-353-400-27
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HYPOTHETICAL: NO. FEFTILE

HYPOTHETICAL: NO.

ANTI-SENSE: NA/A

ANTI-SENSE: NA/A

ANTI-SENSE: NA/A

ANTI-SENSE: NA/A

ANTI-SENSE: NA/A

REAGRENT TYPE: INTERNAL

ORIGINAL SOURCE: NAIO.

ORIGINAL SOURCE: SYNTHESIZED PEPTIDE

POSITION IN GENOME: N/A

FEATURE: SYNTHESIZED PEPTIDE

POSITION IN GENOME: N/A

IDENTIFICATION METHOD: and

IDENTIFICATION METHOD: and

IDENTIFICATION METHOD: and

OTHER INFORMATION: thereby

OTHER INFORMATION: thereby

OTHER INFORMATION: dest is removed and

OTHER INFORMATION: THE INTH AMERICAN

VOLUME: SYMPOSIUM

VOLUME: SYMPOSIUM

VOLUME: SYMPOSIUM

VOLUME: RELEVANT RESIDUES IN TERSUO

TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES

VOLUME: GIOPOLYMERS

VOLUME: GIOPOLYMERS

VOLUME: JOHN WILLEY AND SONS, INC.

ISSUE: JOHN AND SONS, INC.

ISSUED: JOHN AND SONS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5: CYS-SE
STRUCTURE
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: PROCEEDINGS OF THE 11TH AMERICAN
: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-467-472C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.0 Matches 3; Conservative
                      DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE: 1986
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YWLTIW 7
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TITLE: BY
TITLE: TA
JOURNAL:
JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 26; DB 1; Length 8; 60.0%; Pred. No. 3.8e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-467-472C-5
US-08-472C-8

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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/467,472C
FILLING DATE: 6-UUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILLING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILLING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REGISTRATION NUMBER: 27,224
REGISTRATION NUMBER: 27,224
TELECOMMULICATION INFORMATION:
TELEPHONE: (212) 697-3355
APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-JUL-1994
APPLICATION NUMBER: 08/026,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: SUNDEMO,JOHN,S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
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TELEX: NONE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
US-08-415-099A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WLTIW 7.
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PUBLICATION DATE:
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US-09-082-279B-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-082-279B-1500
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JOURNAL:
JOURNAL:
JOURNAL:
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LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: UNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PREFILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: N/A
ANTI-SENSE: N/A
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                                                           Sequence 6, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
    APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; VUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; STATE: NY
; STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ. IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-UNB-1995
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-ANGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-ANUARY-1993
ATTORNEY/ABGNT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEFPAN: ANGUST INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYMPOSIUM
ESCOM (LEIDEN 1990)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: PEPTIDE POTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
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DOCUMENT NUMBER:
FILING DATE:
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VOLUME: I
   RESULT 13
US-08-467-472C-6
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Gaps
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                                                                                                                                                                                                    DOCUMENT NUMBER:
PULLICA DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: NY THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 48.1%; Score 26; DB 3; Length 8; Best Local Similarity 60.0%; Pred. No. 3.8e+05; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 3; Length 8; Pred. No. 3.8e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7972-043
CURRENT APPLICATION NUMBER: US/09/082,279B
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
ITILE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6: CYS-SER
STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN JOURNAL: PEPTIDE JOURNAL: SYMPOSIUM VOLUME: SSCOM (LEIDEN 1990)
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1500
LENGTH: 8
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1500, Application US/09082279B Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-467-472C-6
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Best Local Similarity 50.0%;
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YWLTIW 7
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REBUTA 15

Sequence 5, Application Us/09384061

Sequence 5, Application Us/09384061

Sequence 5, Application Us/09384061

Sequence 6, Application Us/09384061

Sequence 6, Application Us/09384061

SEQUENCE 11 PROPATION: LANTHOUNDE BRIDGED PEPTIDES

COMPRESSER, BROCKE MAINT HAFPER 6 DELAHUNTY

STREET: SPERA AND SERVE AND SECURIOR SETTIONS

STREET: SPERA AND SERVE AND SECURIOR SETTIONS

STREET: SPERA AND SERVE AND SECURIOR SETTIONS

STREET: SPERA AND SETTIONS

COMPUTER SEASON SETTION SETTION SETTIONS

STREET: SPERA AND SETTION SETTION SETTIONS

STREET: SPERA AND SETTION ```

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GapB
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INPORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
UOGNALA: BIOPOLYMERS
UOGNALA: BIOPOLYMERS
UOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DATE: 1986
DATE: 1986
DATE: PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
ADTHORS: BEAN, MARK F.
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: NO THE SYNTHESIS OF A CYCLIC DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.1%; Score 26; DB 3; Length 8; 50.0%; Pred. No. 3.8e+05; tive 1; Mismatches 2; Indels
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STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                       TANDEM MASS SPECTROMETRY
PROCEEDINGS OF THE 11TH AMERICAN
PROPERTINE
SYMPOSIUM
ESCOM (LEIDEN 1990)
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Job time : 38 secs
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
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TITLE: BY
TITLE: TA
JOURNAL:
JOURNAL:
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January 3, 2005, 12:31:17 ; Search time 140 Seconds (without alignments) 20.556 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1599051 segs, 359727711 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq_length: 8
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Semena 67 Appl    |                  | 0                  | Sequence 38, Appl | Sequence 3, Appli | Sequence 5, Appli | Seguence 1655, Ap  | Seguence 9, Appli | Sequence 38, Appl | Sequence 227, App | ~                 | Sequence 227, App | Sequence 227, App |
|-------------------------------|-------------------|------------------|--------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| SUMMARIES                     | 118-10-046-922-67 | US-10-046-922-68 | US-10-351-641-1650 | US-09-884-767A-38 | US-10-433-452A-3  | US-09-852-870A-5  | US-10-351-641-1655 | US-10-196-937A-9  | US-10-457-780-38  | US-10-367-580-227 | US-10-367-593-227 | US-10-367-594-227 | US-10-367-654-227 |
| DB                            | 15                | 13               | 14                 | σ                 | 16                | φ                 | 14                 | 15                | 16                | 15                | 15                | 15                | 15                |
| *<br>Query<br>Match Length DB |                   | - αο             | 60                 | 7                 | 7                 | 80                | æ                  | 8                 | 80                | œ                 | 8                 | 80                | ω                 |
| %<br>Query<br>Match           | 61.1              | 61.1             | 50.0               | 48.1              | 48.1              | 48.1              | 48.1               | 48.1              | 48.1              | 47.2              | 47.2              | 47.2              | 47.2              |
| Score                         | 33                | 33               | 27                 | 26                | 26                | 26                | 26                 | 56                | 56                | 25.5              | 25.5              | 25.5              | 25.5              |
| Result<br>No.                 | -                 | 101              | e                  | 4                 | ß                 | 9                 | 7                  | 60                | 6                 | 10                | 11                | 12                | 13                |

| Sequence 227, App | 2        | 2           | H        | 9       | 4         | ä      | 4      | H      | ä      | 179,              | 7      | 279,   | 133,   | 35, A | 1999  | Sequence 31, Appl | 32,   | 35,   | 19    | 133   | 'n      | 19,               | e 12,   | 49   | 52   | 49     | 52     | 34     | 9    | Sequence 45, Appl |                  |
|-------------------|----------|-------------|----------|---------|-----------|--------|--------|--------|--------|-------------------|--------|--------|--------|-------|-------|-------------------|-------|-------|-------|-------|---------|-------------------|---------|------|------|--------|--------|--------|------|-------------------|------------------|
| ٠,                | 10-367-  | 0-367-674-2 | -09-155- | 190-082 | 190-082-4 | 85     | 5      | 05     | 05     | US-10-050-898-179 | 05     | 9      | 37     | 14    | 14    | 61                | 61    | 7     | 14    | 67    | 47      | US-09-947-925A-19 | 0-386-5 | 5-54 | 436  | 712-42 | 712-42 | 414-52 | 407  | 346-737A-         | US-09-563-222-53 |
| 15                | 15       | 16          | 10       | 14      | 14        | 17     | 14     | 14     | 14     | 14                | 14     | 14     | 14     | 15    | 12    | 15                | 12    | 16    | 16    | 16    | 17      | 6                 |         | 15   | 15   | 16     | 16     | 14     | 14   | 16                | 10               |
| ω                 | σ        | 00          | 'n       | 7       | 7         | 7      | 60     | 00     | æ      | æ                 | æ      | 8      | 80     | œ     | œ     | 80                | œ     | œ     | ۵     | æ     | 9       | 80                | 4       | 2    | 'n   | S      | Ŋ      | 9      | 9    | 9                 | 7                |
| 5.5 4             | 25.5 47. | 25.5        | 25 46.   | 25 46.  | 25 46.    | 25 46. | 25 46. | 25 46. | 25 46. | 25 46             | 25 46. | 25 46. | 25 46. | 25 4  | 25 46 | 25 46             | 25 46 | 25 46 | 25 46 | 25 46 | 24.5 45 | 24.5 4            | 24 44   | 24 4 | 24 4 | 24 4   | 24 44  | 24 4   | 24 4 | 24 44.4           | 4                |
| 14                | 15       | 16          | . 17     | 18      | 13        | 20     | 21     | 22     | 23     | 24                | 25     | 56     |        |       |       | 30                | 31    | 32    | 33    | 34    | 35      | 36                | 37      | 38   | 39   | 40     | 41     | 42     | 43   | 44                | 45               |
|                   |          |             |          |         |           |        |        |        |        |                   |        |        |        |       |       |                   |       |       |       |       |         |                   |         |      |      |        |        |        |      |                   |                  |

## ALIGNMENTS

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US-10-046-922-67

US-10-046-922-67

Sequence G7, Application US/10046922

Publication No. US2020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Alitalo, Kari

APPLICANT: Alitalo, Kari

APPLICANT: Rubo, Hajime

TITLE OF INVENTION: VEFER-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 2896-7/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PATENTE: A PATENTIAL OF SEQ ID NOS: 80

SOFTWARE: PATENTE: TENGRALION: X at position 4-6 is any amino acid

UCATION: (4)..(6)

OTHER INFORMATION: X at position 4-6 is any amino acid

US-10-046-922-67

QUETY MATCh

BEST LOCAL SIMILARITY 57.1%; Pred: No. 1.5e+06;

MATCH G1 | | | | | |

DD I GYMXXXM 7
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RESULT 2 US-10-046-922-68 ; Sequence 68, Application US/10046922

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US-09-884-767A-38
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Publication No. US20030186874A1

GENERAL INCOMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Meritka, G.

APPLICANT: Meritka, G.

APPLICANT: Meritka, G.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRE: US/10/351,641

FILE REFERENCE: 7872-100

CURRENT FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 1757

SCOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alicalo, Kari
APPLICANT: Alicalo, Kari
APPLICANT: Kolvunen, Erki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/371084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 27; DB 14; Length 8; 50.0%; Pred. No. 1.5e+06; 1ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.1%; Score 33; DB 13; Length 8; 57.1%; Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (4)..(6)
OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (8) ...(8) CTHER INFORMATION: X is any amino acid US-10-046-922-68
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Matches 4; Conservative
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Best Local Similarity
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1 WDSLWG 6
                                                                                                                                                                                                                                                                                                                     ORGANISM: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-351-641-1650
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-10-351-641-1650
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LENGTH: 8
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                                                                                                                                                                                                                                                                                             TYPE: PRT
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RESULT 4 US-09-884-767A-38

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NAME/KEY: VARIANT
LOCATION: (1)..(1).
OTHER INFORMATION: Xaa is R or a large hydrophobic amino acid, e.g. phenylalanine:
OTHER INFORMATION: F, tyrosine: Y, or tryptophan: W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                        APPLICANT: Ley, Arthur C.
APPLICANT: Louneau, Christopher J.
APPLICANT: Luneau, Christopher J.
APPLICANT: Luneau, Christopher J.
TITLE OF INVERVION: NOVEL ENTEROXINASE CLEAVAGE SEQUENCES; TITLE OF INVERVION: NOVEL ENTEROXINASE CLEAVAGE SEQUENCES; FILE REFERENCE: DXX-012.1 US, DXX-012.1 PCT
CURRENT APPLICATION NUMBER: US/09/884,767A
CURRENT FILING DATE: 2001-06-19
PRIOR PILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: ABBLICATION OF SEQ ID NOS: 217
LENGTH: ABBLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic enterokinase cleavage sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.1%; Score 26; DB 9; Length 7; Best Local Similarity 75.0%; Pred. No. 1.5e+06; Matches 3; Conservative 1; Mismatches 0; Indels
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PUBLICACE 3, Application US/10433452A

PUBLICACE 3, Application US/10433452A

PUBLICACE 3, Application US/10433452A

GENERAL INFORMATION:
APPLICANT: Brekke, Ole Henrik
APPLICANT: Bandlie, Inger

TITLE OF INVENTION: Hybrid Antibodies
FILE REFERENCE: DEH-0014

CURRENT APPLICATION NUMBER: US/10/433,452A

CURRENT PILING DATE: 2003-11-24

PRIOR FILING DATE: 2000-12-01

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PALENTIN VERSION 3.2

SEQ ID NO 3

LENGTH: 7
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Sequence 38, Application US/09884767A Publication No. US20020192789A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                               APPLICANT: DYAX Corp
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWL 4
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; Sequence 1655, Application US/10351641
; Publication No. US2030186874A1
; GENERAL INFORMATION:
A APPLICANT: Barney, S.
A APPLICANT: Anwer, M.
A APPLICANTON: PROBERTIES
FILE REFERENCE: 703-2-00
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT APPLICATION NUMBER: 09/350,641
FRIOR FILING DATE: 1999-05-20
FRIOR APPLICATION NUMBER: 09/315,304
FRIOR FILING DATE: 1999-05-20
FRIOR FILING DATE: 1998-05-20
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Pred. No. 1.5e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 9; Length 8;
Pred. No. 1.5e+06;
1; Mismatches 2; Indels
             Sequence 5, Application US/09852870A
Patent No. US20020165132A1
GENERAL INFORMATION
APPLICANT: Goodman, Murray
APPLICANT: Goodman, Murray
APPLICANT: Osapay, George
FILLE OF INVENTION: Lanchionin Bridged Proteins
FILLE OF INVENTION Lanchionin Bridged Proteins
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT FILING DATE: 2001-05-10
FRIOR APPLICATION NUMBER: US 09/384,601
FRIOR APPLICATION NUMBER: US 09/384,601
FRIOR APPLICATION NUMBER: US 09/384,601
FRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Cys-Ser lanthionine bridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0°
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Best Local Similarity 60.0
Matches 3; Conservative
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FWKTSW 8
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; ORGANISM: HIV-1
US-10-351-641-1655
-09-852-870A-5
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RESULT 8 US-10-196-937A-9

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US-LO-427-V-80-38

Sequence 38, Application US/1045780

Publication No. US20040137426A1

GENERAL INFORMATION:
APPLICANT: SERRES, Pierre-Francois
APPLICANT: MOSCA, Joseph
TITLE OF INVENTION: OT TARGET CELLS
TITLE OF INVENTION: TO TARGET CELLS
TITLE OF INVENTION: TO TARGET CELLS
TITLE OF INVENTION: TO TARGET CELLS
CURRENT APPLICATION NUMBER: US/10/457,780

CURRENT APPLICATION NUMBER: US 60/446,268
PRIOR PLING DATE: 2003-02-11
PRIOR PLING DATE: 2003-02-11
PRIOR PLING DATE: 2003-02-11
PRIOR PLING DATE: 2002-09-27

PRIOR APPLICATION NUMBER: US 60/413,919

PRIOR APPLICATION NUMBER: US 60/386,754

PRIOR PLING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn version 3.2

SEQ ID NO 38

LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 4 - OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
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                    PUBLICACION NO. US20040024176A1
GENERAL INPORMATION:
TITLE OF INVENTION: CYCLIC Peptide Tube
FILE REFERENCE: 397.2 Div 1/SCR 2381
CURRENT APPLICATION NUMBER: US/10/196,937A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 08/632,444
PRIOR PILING DATE: 1996-04-15
PRIOR PILING DATE: 1996-04-15
PRIOR FILING DATE: 1994-10-11
PRIOR FILING DATE: 1993-10-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PSELSEQ for Windows Version 4.0
SSOFTWARE: PSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Length: 8 amino acids OTHER INFORMATION: Type: amino acids OTHER INFORMATION: Topology: Circular
Sequence 9, Application US/10196937A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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LOCATION: 8
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1 WLWLW 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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RESULT 12

US-10-567-594-227

Sequence 227, Application US/10367594

Publication No. US20040071722A1

GENERAL INFORMATION:

APPLICANT: Rothman, James E.

APPLICANT: Harll, F. Ulrich

APPLICANT: Hach, Mee H.

APPLICANT: ARechi, Yoshizumi

APPLICANT: Houghton, Alan

APPLICANT: Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFREENCES: 11746/461041

CURRENT APPLICATION NUMBER: US/10/367,594

CURRENT PILING DATE: 2003-02-14

PRIOR FILING DATE: 1998-02.13

PRIOR PAPLICATION NUMBER: PCT/US96/13363

PRIOR PAPLICATION NUMBER: DCS/0002,490

PRIOR FILING DATE: 1996-08-18

PRIOR PILING DATE: 1996-08-18

PRIOR PILING DATE: 1996-08-18

PRIOR PILING DATE: 1995-08-18

PRIOR PILING DATE: 1995-08-18

PRIOR PLING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SEQ ID NO 227

LENGTH: WADDEL CATH SEC ID NOS: 349

SEQ ID NO 227

LENGTH: WADDEL CATH SEC ID NOS: 349

TUDEN DATE: US SEC ID NOS: 349

LENGTH: BATE DE SEC ID NOS: 349

LENGTH: WADDEL CATH SEC ID NOS: 349

LENGTH: BATE DE SEC ID NOS: 349
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Pred. No. 1.5e+06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.2%; Score 25.5; DB 15;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0;
PRIOR APPLICATION DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 09/011,645

PRIOR PILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: PCT/US96/13363

PRIOR APPLICATION NUMBER: US 60/002,490

PRIOR APPLICATION NUMBER: US 60/002,470

PRIOR APPLICATION NUMBER: US 60/002,479

PRIOR FILING DATE: 1995-08-18

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 227

LENGTH: 8

LENGTH: 8
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, OTHER INFORMATION: synthetic peptide
US-10-367-594-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: synthetic peptide US-10-367-593-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative ;
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1 GWWVT-W 6
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Sequence 227, Application Wo. US20046071720A1

GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Yoshizumi
APPLICANT: Houghton, Yoshizumi
APPLICANT: Maybew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461061
CURRENT APPLICATION NUMBER: US/10/367,580
CURRENT FILING DATE: 2003-02-14
FRIOR APPLICATION NUMBER: US 09/011,645
PRIOR PELING DATE: 1998-02-13
PRIOR PILING DATE: 1996-02-13
PRIOR PELING DATE: 1996-08-16
PRIOR PELING DATE: 1995-08-18
PRIOR PELING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ 1D NOS: 349
PRIOR FILING DATE: 1995-08-18
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APPLICANT: Hartl, F. Ulrich
APPLICANT: How, Mee H.
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/4461012
CURRENT APPLICATION NUMBER: US/10/367,593
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47.2%; Score 25.5; DB 15; Length 8; Best Local Similarity 57.1%; Pred. No. 1.5e+06; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                               48.1%; Score 26; DB 16; Length 8; 60.0%; Pred. No. 1.5e+06; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthetic peptide US-10-367-580-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 227, Application US/10167593; Publication No. US20040071721A1; GENERAL INFORMATION:
                                    ; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: r-W8F
US-10-457-780-38
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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GWWVT-W 6
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US-10-367-593-227
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LENGTH: 8
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                                                                                                                                GREEAL INFORMATION:

APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: How, Mee H.

APPLICANT: How, Mee H.

APPLICANT: Houghton, Alan

APPLICANT: Houghton, Alan

APPLICANT: Mayhew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REPEBROCE: 11746/461022

CURRENT PILION INMBER: US/10/367,654

CURRENT APPLICATION NUMBER: US 10/171,734

PRIOR APPLICATION NUMBER: US 09/6136,295

PRIOR PRILING DATE: 2000-06-13

PRIOR PILING DATE: 1996-02-13

PRIOR PLILING DATE: 1996-03-16

PRIOR PLILING DATE: 1996-08-16

PRIOR FILING DATE: 1996-08-16

PRIOR PLILING DATE: 1996-08-16

PRIOR PLILING DATE: 1996-08-16

PRIOR PLILING DATE: 1996-08-16

PRIOR PLILING DATE: 1995-08-18

PRIOR PELING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SEQ ID NO 227

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US-1U-36, PS-84-27,
US-1U-36, PS-84-27,
Publication No. US20040071724A1
GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Howighton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
ITILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 17746/461051
CURRENT APPLICATION NUMBER: US 09/794,529
FRIOR APPLICATION NUMBER: US 09/794,529
FRIOR FILING DATE: 1998-02-17
FRIOR FILING DATE: 1998-02-16
FRIOR FILING DATE: 1996-08-16
FRIOR FILING DATE: 1996-08-16
FRIOR FILING DATE: 1995-08-18
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Pred. No. 1.5e+06;
2; Mismatches 0;
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Sequence 227, Application US/10367654 Publication No. US20040071723A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
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GWWVT-W 6
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SERVERAL INFORMATION:

APPLICANT: Rothman, James E.

APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: Houghton, Alan

APPLICANT: Maybew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFERENCE: 11746/461072

CURRENT APPLICATION NUMBER: US 103/794,517

PRIOR APPLICATION NUMBER: US 09/794,517

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1996-08-18

PRIOR PILING DATE: 1995-08-18

PRIOR FILING DATE: 1995-08-18

PRIOR FILING DATE: 1995-08-18

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SOFTWARE: WordPerfect 8.0 for Windows

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                                                                                                                                                    1 Similarity 57.1%; Score 25.5; DB 15; Similarity 57.1%; Pred. No. 1.5e+06; 4; Conservative 2; Mismatches 0;
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                                                ; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-227
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 227, Application US/10367668 Publication No. US20040071725A1 GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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1 GWWVT-W
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

January 3, 2005, 12:22:35; Search time 38 Seconds (without alignments) 20.256 Million cell updates/sec Run on:

SEQ32 54

1 gywltiwg 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:`

909

Minimum DB seq length: 0 «MaximumwDBmseqmlength:編8]]

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| IES       | Description    | T-cell receptor be | qut pentapeptide . | leucokinin V - Mad | T-cell receptor be | _      | _      | ದ      | l recepto: | receptor |        | T-cell receptor be | glucuronosyltransf | major fat-globule | pev-kinin 1 - pena | triacylglycerol li | neuromodulatory pe | neuromodulatory pe |        | œ)     | leucokinin VI - Ma | leucokinin VII - N | leucokinin VIII - | angiotensin-conver | hypothetical prote | T-cell receptor be | T-cell receptor ga | - dest | Ig H chain V-D-J |
|-----------|----------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|------------|----------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|------------------|
| SUMMARIES | Ω              | PT0586             | JH0253             | JS0315             | B53284             | PT0629 | PT0637 | A61068 | PT0628     | PT0642   | PT0722 | PT0728             | PX0008             | B48394            | PD0029             | S57274             | 533244             | S33245             | S33246 | PT0724 | JS0316             | JS0317             | JS0318            | A31570             | 809652             | PT0532             | F41946             | A58725 | PH1618           |
|           | 08             | . 0                | ~                  | ~                  | ~                  | ~      | ~      | ~      | ~          | ~        | 7      | 7                  | 7                  | ~                 | ~                  | ~                  | ~                  | ~                  | ~      | ~      | ~                  | ~                  | ~                 | ~                  | ~                  | N                  | ~                  | 4      | ~                |
|           | Length DB      | 7                  | Ŋ                  | 80                 | 4                  | 9      | 9      | 9      | 7          | 7        | 7      | 7                  | 7                  | . 7               | 7                  | 7                  | 7                  | 7                  | 7      | 80     | 80                 | ω                  | 80                | 80                 | 7                  | 9                  | 9                  | 7      | 80               |
|           | Query<br>Match | 40.7               | 37.0               | 33.3               | 31.5               | 31.5   | 31.5   |        |            | 31.5     | 31.5   | 31.5               | 31.5               | 31.5              | 31.5               | ä                  | 31.5               |                    | 31.5   | 31.5   | 31.5               | 31.5               | н                 | 31.5               | 29.6               |                    | 27.8               | 27.8   | 27.8             |
|           | Score          | 22                 | 20                 | 18                 | 17                 | 17     | 17     | 17     | 17         | 17       | 17     | 17                 | 17                 | 17                | 17                 | 17                 | 17                 | 17                 | 17     | 17     | 17                 | 17                 | 17                | 17                 | 16                 | 15                 | 15                 | 15     | 15               |
|           |                | -                  | 7                  | ٣                  | 4                  | s      | 9      | 7      | 80         | 6        | 10     | 11                 | 12                 | 13                | 14                 | 15                 | 16                 | 17                 | 18     |        | 50                 |                    |                   | 23                 | 24                 | 25                 | 26                 | 27     | 28               |

| cytochrome oxidase dihydrofolate redu cerebellar degener | T-cell receptor be<br>dermorphin (Trp-4,<br>Ig H chain V-D-1 r<br>tubulin beta-3 cha | globulin IV alpha<br>cholecystokinin-5<br>dnaA protein - Pse<br>dihydxofolate redu | ameletin - rat<br>dermorphin - Rohde<br>fatty-acid synthas<br>glutathione transf<br>dermorphin (Lys-7) |
|----------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|
| T13818<br>A31263<br>B35640                               | PT0519<br>S21230<br>PH1602<br>S33567                                                 | S09478<br>A32516<br>B34835<br>B31263                                               | A61411<br>A61324<br>A60139<br>S71870<br>S36662                                                         |
| 000                                                      | 0000                                                                                 | 0000                                                                               | 88858                                                                                                  |
| 27.8<br>25.9<br>6                                        | 25.9<br>25.9<br>7<br>25.9                                                            | 24.1<br>24.1<br>24.1<br>6                                                          | 24.1<br>24.1<br>24.1<br>24.1<br>7<br>24.1<br>7                                                         |
| 11<br>14<br>14                                           | 1 1 1 1<br>4 4 4 4                                                                   | 13<br>13<br>13                                                                     | 13<br>13<br>13                                                                                         |
| 30                                                       |                                                                                      | # # # # # # # # # # # # # # # # # # #                                              | 4 4 4 4 4<br>4 5 6 4 5                                                                                 |

## ALIGNMENTS

PT0586
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558

A; Status: translation not shown

A;Molecule type: mRNA A;Residues: 1-7 <FRES. Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD) C;Keywords: T-cell receptor

Gaps ö 0; Indels Length 7; Score 22; DB 2; I Pred. No. 2.8e+05; 1; Mismatches Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative 1

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:||| 3 SIWG 6 5 TIWG 8 ઠે . 엄

gut pentapeptide - Japanese eel

A;Molecule type: protein A;Residues: 1-5 <UES> A;Experimental source: gut C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastr , and of the circular muscle of the gastro-intestinal junction.

ö Query Match
37.0%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels

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Gaps

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C;Accession: A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, prin
A;Reference number: A61068; MUID:92262881; PMID:1585017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0637
A;Status: translation not shown
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0637
R;Peeney, A.J.
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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A;Residues: 1-6 <SCH>
A;Cross-references: UNIPROT:P41491
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB C;Keywords: T-cell receptor
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                                                                                                                    DB 2; Le
2.8e+05;
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A;Residues: 1-6 cFEB.
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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Best Local Similarity
Matches 2; Conserv
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PT0637
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A,Residues: 1-8 <HOL>
A,Cross-references: UNIPROT:P19987
C,Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C,Keywords: amidated carboxyl end, cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                            C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990
C;Date: 07-Sep-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
A) Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and A;Reference number: A53284; MUID:91342695; PMID:1678859
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A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-4 <HAR>
A;Cross-treferences: GB:S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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                                                    JS0315
leucokinin V - Madeira cockroach
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A;Molecule type: mRNA
A;Residues: 1-6 <FE2>
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A, Status: translation not shown
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Matches 2; Conservative
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A; Residues: 1-6 <FEE>
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R;Yokota, H.; Yuasa, A.; Sato, R.
2. Biocham. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver m
A;Reference number: PX0008; MUID:89197852; PMID:3149280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
        C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
F;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0728
A;Accession: PT0728
A;Accession: PT0728
A;Accession: PT0728
A;Experimental not shown
A;Molecule type: DNA
A;Redules: 1-7 FEBS-
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucuronosyltransferase (BC 2.4.1.17), hepatic - rat (fragment)
NiAlternate names: UDP-glucuronyltransferase
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
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A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: PX0008
A;Molecule Lype: protein
A;Residues: 1-7 < VOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    II-like sequences.
A; Reference number: A48394; MUID:93250576; PMID:8485470
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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Pred. No. 2.8e+05;
1; Mismatches 1;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Pro642
T-Cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Jocession: Pro642
T-Cell 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: Pro642
T. Exp. Med. 174, 115-124, 1991
A.Fielency, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Fielency number: Pro509; MUID:91277601; PMID:1711558
A.Fielence number: Pro642
A.Status: translation not shown
A.Status:
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C; Species Ms musculus (house mouse)
C; Species ins musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0722
J Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MVID:91277601; PMID:1711558
A; Reference number: PT0509; MVID:91277601; PMID:1711558
A; Recession: PT0722
A; Status: translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-7 <FEE>
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
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31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0628
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <PEE>
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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Matches 2; Conservative
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RESULT 11

ઠ 셤 PT0728

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RESULT 15
S57274
S57274
C;riacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C;Species: Psychrobacter immobilis
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57274
C;Accession: S57274
S;Arple: Corrigendum to "Cloning, sequence and structural features of a lipase from the A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the A;Accession: S57274
MinD: 95359197; PMID: 7632728
A;Reference number: S57274
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Koss-references: UNIPROT: Q02104; EMBL: X67712
C;Keywords: carboxylic ester hydrolase
                                              Portain 1 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Species: Penaeus vannamei
C;Species: Penaeus vannamei
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C;Accession: PD0029
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devreese, Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Reference number: PD0027; MUID:98342103; PMID:9675150
A;Accession: PD0029
A;Accession: PD0029
A;Accession: PD0029
A;Residues: 1-7 <NIE>
C;Comment: This peptide belongs to myotropic neuropeptides.
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31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 2; Conservative
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RESULT 14
PD0029
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Search completed: January 3, 2005, 12:31:54 Job time : 39 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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protein search, using sw model OM protein

Run on:

January 3, 2005, 12:14:40 ; Search time 189 Seconds (without alignments)
24.354 Million cell updates/sec

Title: Perfect score:

1 gywltiwg 8 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

835 Total number of hits satisfying chosen parameters:

Minimum

Minimum DB seq length: 0
Maximum DB-seq-length:-8-7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | uo                    | fuerstia af | fuerstia | homo sapi | human immun | mus musculu   | leucophaea | periplaneta | rattus norv | locusta mig | achatina fu | achatina fu | achatina fu | glycine max | thunnus alb | eucophaea | eucophaea | eucophaea | eucophaea | eucophaea  | leucophaea | leucophaea | periplaneta | periplaneta | periplaneta | periplaneta | s taurus   | plectranthu | branchiosto | silene coni | lychnis cor | plectrant  |
|-----------|-----------------------|-------------|----------|-----------|-------------|---------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-----------|-----------|-----------|-----------|------------|------------|------------|-------------|-------------|-------------|-------------|------------|-------------|-------------|-------------|-------------|------------|
|           | Description           | Q70y57 fu   |          | Aab33374  |             | _             |            |             |             |             | -           |             |             |             | _           | 7         | 7         | _         | ٦         | _          |            |            |             |             |             | _           |            |             |             |             |             | Cad45500   |
| SUMMARIES | , OI                  | Q70Y57      | CAD45547 | AAB33374  | 08JE81      | UF01 MOUSE    | LCK5_LEUMA | PK4_PERAM   | Q62721      | LOK1_LOCMI  |             | WWA2_ACHFU  | WWA3_ACHFU  | 049223      |             |           | 1 1       |           |           | LCK6_LEUMA | LCK7_LEUMA |            |             | PK2_PERAM   |             |             | RT34_BOVIN | Q70Y84      | Q7GEM6      | 062201      | 062202      | CAD45500   |
|           | DB                    | ~           | ~        | N         | N           | <del></del> 1 | Н          | Ч           | 7           | H           |             | Н           | Н           | ~           | Н           | н         | -         | -         | Т         | -          | -          | ٦          | 7           | 7           | -1          | -           | ~          | N           | ~           | ~           | ~           | 7          |
|           | Query<br>Match Length | 80          | æ        | 80        | 7           | ហ             | 80         | æ           | 80          | 9           | 7           | 7           | 7           | 7           | 80          | œ         | 80        | 80        | œ         | 80         | 60         | 80         | 60          | 80          | 80          | æ           | 8          | 8           | 80          | 80          | œ           | <b>c</b> o |
| d         |                       | 4           | 48.1     | 38.9      | 37.0        | 35.2          | 33.3       | 33.3        | 33.3        | 31.5        | 31.5        | 31.5        | 31.5        | 31.5        | 31.5        | 31.5      | 31.5      | ٠         | •         | ٠          | ٠          | 31.5       | •           | 31.5        | •           | 31.5        | 31.5       | 31.5        | ٠           | 31.5        | 31.5        | 31.5       |
|           | Score                 | 26          | 26       |           |             | 19            |            | 18          | 18          | 17          | 17          | 17          | 17          | 17          | 17          | 17        | 17        | 17        | 17        | 17         |            | 17         | 17          | 17          | 17          | 17          | 17         | 17          | 17          | 17          | 17          | 17         |
|           | Result<br>No.         | -           | 7        | e         | 4           | ß             | 9          | 7           | 8           | σ           | 10          | 11          | 12          | 13          | 14          | 15        | 16        | 17        | 18        | 19         | 20         | 21         | 22          | 23          | 24          | 25          | 56         | 27          | 28          | 59          | 30          | 31         |

| Cag24877 lychnis c<br>Cag24879 silene co<br>P82096 litoria rub<br>Q9bry4 homo sapien<br>085406 coxiella bu<br>P58649 octopus min<br>P88853 mus musculu<br>Q71515 varanus tin<br>094v91 varanus tin<br>Q94v92 varanus sal<br>Q94vb2 varanus sal<br>Q94vb2 varanus sal<br>Q94vb2 varanus sal |
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| CAG24877 CAG24879 CAG24879 09BRT4 085406 OCP3_OCTMI O715_5 0915_6 094V91 094VB5 094VB5                                                                                                                                                                                                     |
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| 311.5<br>229.66<br>229.66<br>227.78<br>227.78<br>227.78<br>227.88<br>227.88                                                                                                                                                                                                                |
| 117<br>117<br>118<br>118<br>118<br>118<br>118<br>118<br>118                                                                                                                                                                                                                                |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                      |

## ALIGNMENTS

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Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
                                                                                                           Chloroplast.

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Lamiales, Lamiaceae, Nepetoideae, Ocimeae, Fuerstia.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                         based on three plastid DNA regions.";

Mol. Phylogenet. Evol. 31:277-299(2004).

GOS. GOS.0003735; CAD45547.1; -.

GOS. GOS.0003735; F.structural constituent of ribosome; IEA.

Ribosomal protein.

NON TER

S SEQÜENCE 8 AA, 916 MW; DABEABS8637041B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 100.0%; Pred. No. 1.8e+06; 4; Conservative 0; Mismatches 0; Indels
                        05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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PRT;
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14-MAR-2004 (TEEMBLEEL: 27, La
14-MAR-2004 (TEEMBLEEL: 27, La
Ribosomal protein (Fragment):
RPS16.
                                                                    Ribosomal protein (Fragment)
Name=rps16;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                [1] SEQUENCE FROM N.A. PubMed=15019625;
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                               Fuerstia africana.
                                                                                                                                                                  NCBI_TaxID=204226,
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Q70Y57
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Chloroplast.
Eukaryoch; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
NCBI\_TaxID=204226;

Fuerstia africana.

N

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Gaps

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TISSUE=Head;
MEDLINE=87052651; PubMed=2877794;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
Isolation, primary structure, and synthesis of leucokinins V and VI:
myotropic peptides of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:27-30(1987).
-:- FUNCTION: This cephalomyotropic peptide stimulates contractile
"Diversity and complexity of HIV-1 drug resistance: a bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; AF347267; AAX32344.1; -.
1 1 SEQÜENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leucophaem maderae (Madeira cockroach).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
                                                                                                                                                      Score 20; DB 2; Length 7; Pred. No. 1.8e+06; 2; Mismatches 0; Indels
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Pred. No. 1.8e+06;
1; Mismatches 2; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Leucokinin V (L-V).
                                                                                                                                                                                                                                                                                                                                                                                                   5 AA.
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                                                                                                                                                             37.0%;
50.0%;
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Best Local Similarity
Matches 2; Conserv
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3 ITLW 6
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LCK5_LEUMA
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UF01 MOUSE
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                                                 Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL, AJSO5427, CAD45547.1; -. Chloroplast; Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=95156893; PubMed=7853788;
MRDLINE=95156893; PubMed=7853788;
MRDLINE=95156893; PubMed=7853788;
Takada T., Yoshicka K., Endo F., Matsuda I.;
"Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in primordial germ cells.";
Kidney Int. 46:1307-1314(1994).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T., Hoffmann D., Korn K., Selbig J.;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Collagen alpha 5(IV) chain (Fragment).
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                              8 AA; 916 MW; DABEAB58637041B5 CRC64;
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40.0%; Pred. No. 1.8e+06;
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Best Local Similarity
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SEQUENCE FROM N.A.
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2 TIWG 5
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SEQUENCE.
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WWA1_ACHFU
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-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                       Gaps
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-!- MASS SPECTROMETRY: MW=838.15; METHOD=Electrospray; RANGE=1-8; NOTE=Ref.1.
-!- SIMILARITY: Belongs to the kinin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predel R., Kellner R., Rapus J., Penzlin H., Gade G., Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Periplaneta americana (American cockroach).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Nooptera, Orthopteroidea, Dictyoptera; Blattaria, Blattoidea, Blattidae, Periplaneta.
                                                                                                                                                     Similarity 37.5%; Pred. No. 1.8e+06; 3; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%; Score 18; DB 1; Length 8; 37.5%; Pred. No. 1.8e+06; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
TISSUE-Corpora cardiaca;
MEDLINE-98010462; PubMed-9350979;
activity of cockroach protodeum (hindgut).
-1- SUBCELLULAR LOCATION: Secreted.
PIR, JS0315, JS0315.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
8 Glycine amide.
SEQÜENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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MOD RES 8 Glycine amide.

SEQUENCE 8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-4 (Pea-K-4).
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MEDLINE=95331633; PubMed=7607556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity).
SUBCELLULAR LOCATION:
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Best Local Similarity 37.5-
Best Local Similarity 37.5-
3; Conservative
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Rattus norvegicus (Rat)
                                                                                                                                                                         Best Local Similarity
Matches 3; Conservat
                                                                                                                                                                                                                                              1 GYWLTIWG 8
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P82688;
                                                                                                                                                         Query Match
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PK4 PERSAM
ID PRK4 PERSAM
AC P82581
DT 05-JUJ
DE RAPID
OC BUART
OC B
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"Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
---- FUNCTION: Myotropic peptide. May be important in the stimulation of ion transport and inhibition of diuretic activity in Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Wwamide-1.
Wwamide-1.
Achatina fulica (Giant African snail).
Eukaryota; Metzazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Sigmurethra; Achatinoidea; Achatina.
                                                                                                                                                                                                                                                                                                                                                    Gaps
Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
Henderson I., Owens G.A., Danner D.B., Jupe B.R., Dell'Orco R.T.,
                                                                                 "Regions of evolutionary conservation between the rat and human prohibitin-encoding genes.";
Gene 158:291-294(1995).
GENEL, U17178; AAA86692.1; -..
NON TER 8 AA, 1150 MW; EFD3237B05A41376 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIŜSUE=Corpora cardiaca;
MEDLINE-92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
                                                                                                                                                                                                                                                                                              Length 8;
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PIR, A61068, A61068.

Andidation; Direct protein sequencing; Neuropeptide.

MOD RES

SEQÜENCE 6 AA; 654 MW; 686165A5B9CDB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.8e+06;
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40.0%; Pred. No. 1.8e+06;
tive 1; Mismatches 2;
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Best Local Similarity 40.0
Matches 2; Conservative
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Angiotensin-converting enzyme inhibitor.
Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosteni; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei; Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
01-DCC-2001 (Fregment)
Glycine max (Soybean).
Glycine max (Soybean).
Glycine max (Soybean).
Subaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Butaryota, Viridiplantae, Streptophyta, Embryophyta;
Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBL TaxID=3847;
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"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
Nucleic Acids Res. 19:4769-4769(1991),
"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
PIR, 533244; S33244.
MOD RES

SEQÜENCE 7 AA, 965 MW; 7362D5B69B132310 CRC64;
                                                                                                                                                                                                 h 31.5%; Score 17; DB 1; Length 7; Similarity 25.0%; Pred. No. 1.8e+06; 1; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%; Score 17; DB 2; Length 7; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;
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TISSUE=Roots;
MEDLINE=91367679; PubMed=1891369;
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Best Local Similarity
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Best Local Similarity
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TISSUE=Muscle;
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P18691;
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ACI_THUAL
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Bukaryota, Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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MEDLINE-93265912; PubMed=8495720;
MEDLINE-93265912; PubMedea Y., Kobayashi M., Nomoto K.;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
PEBS Lett. 323:104-108(1993).
PIR; 833246; 833246.
                                 MEDIINE=93265912; PubMed=8495720; Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the Arrican giant snail, Achatina fulica."; FEBS Lett. 323:104-108(1993).
-: FUNCTION: Exhibits modulatory effects on the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
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                                                                                                                                                                                                                                                                                                                                  Query Match 31.5%; Score 17; DB 1; Length 7; Best Local Similarity 25.0%; Pred. No. 1.8e+06; Matches 1; Conservative 3; Mismatches 0; Indels
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                                                                                                                                                             system. Inhibits activity on a central neuron. PIR, 533245; S33245. Amidation; Direct protein sequencing; Neuropeptide. MOD_RES
                                                                                                                                                                                                                                                            7 7 T Tryptophan amide.
7 AA; 993 MW; 7362D5B69B041310 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Www.mide-2.
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01-07UN-1994 (Rel. 29, Last sequence update)
05-07UL-2004 (Rel. 44, Last annotation update)
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4 MSVW 7
               TISSUE=Ganglion;
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4 MSVW 7
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WWA3_ACHFU
ID WWA3_ACHFU
AC P35921;
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WWA2 ACHFU
ID WWA2 ACHFU
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Holman G.M., Cook B.J., Nachman R.J.;
Holation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
Comp. Biochem. Physiol. 84C:205-211(1986).
-:- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach protodeum (hindgut).
-:- SUBCELLULAR LOCATION: Secreted.
Amidation; Direct protein sequencing; Neuropeptide.
MOD_RES
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MEDLINE-88326322; PubMed-3415688;
Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
"Isolation of angiotensin-converting enzyme inhibitor from tuna
                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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31.5%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                          muscle.";
Biochem. Biophys. Res. Commun. 155:332-337(1988).
-!-FUNCTION: Inhibits angiotensin-converting enzyme.
PIR; A31570, A31570.
Direct protein sequencing; Metalloprotease inhibitor.
SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;
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8 AA; 893 MW; DC6365B449CDC76A CRC64;
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TISSUE-Head;
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